

Result No.	Score	Query Match	Length	DB	ID	Description
1	129	100.0	600	9	US-09-816-391A-1	Sequence 1, Appl1
2	28.4	22.0	536	10	US-09-903-410-31	Sequence 31, Appl1
3	28.4	22.0	936	13	US-10-027-805-31	Sequence 31, Appl1
4	28.4	22.0	936	14	US-10-027-804-31	Sequence 31, Appl1
5	28.4	22.0	2451	10	US-09-938-842A-64	Sequence 64, Appl1
6	27.8	21.6	2037	12	US-10-139-672-591	Sequence 591, Appl1
7	27.8	21.6	2037	12	US-10-187-749-591	Sequence 591, Appl1
8	27.8	21.6	2037	12	US-10-194-457-591	Sequence 591, Appl1
9	27.8	21.6	2037	13	US-10-052-586-591	Sequence 591, Appl1
10	27.8	21.6	2037	14	US-10-174-590-591	Sequence 591, Appl1
11	27.8	21.6	2037	14	US-10-176-758-591	Sequence 591, Appl1
12	27.8	21.6	2037	14	US-10-175-737-591	Sequence 591, Appl1
13	27.8	21.6	2037	14	US-10-173-706-591	Sequence 591, Appl1
14	27.8	21.6	2037	14	US-10-175-728-591	Sequence 591, Appl1
15	27.8	21.6	2037	14	US-10-175-752-591	Sequence 591, Appl1
16	27.8	21.6	2037	14	US-10-176-482-591	Sequence 591, Appl1

OY	1	TGACCTTTGCTCGAGCATTACTTCAGAGATTCTGAGACGAAAGCCCCGACGAGA	60
	472	TGACCTTTCGCTCGAGCATTACTTCAGAGATTCTGAGACGAAAGCCCCGACGAGA	531
Db			
OY	61	TGTCGGGGCTCTTTTGTGTGCTGCTGAGCGTGTGCCACCGATTATTTCGGA	120
	532	TGTCGGGGCTCTTTTGTGTGCTGCTGAGCGTGTGCCACCGATTATTTCGGA	591
Db			

FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: HAILE, LISA A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 09010/010001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-678-5070
 TELEFAX: 619-678-5099
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 936 NUCLEOTIDES
 TYPE: NUCLEIC ACID
 STRANDEDNESS: SINGLE
 TOPOLOGY: LINEAR
 MOLECULE TYPE: GENOMIC DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Query Match 22.0%; Score 28.4; DB 14; Length 936;
 Best Local Similarity 56.4%; Pred. No. 2.3; Mismatches 41; Indels 0; Gaps 0;
 Matches 53; Conservative 0;

2 GACCTCTCTGCTAGCATTACTGAGCATTACTGAGCAGCAAGACCCCGCAGAT 61
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 718 GACCTTGAGAACCTACTCTCTGCGCGATCATTAACCGCGAATAACGCCGCTGAGAGAT 77
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 62 GCTCGGGGCTCTTTTGTGTGCTGCTGACGTG 95
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 778 GAAGGAGAGATTTCGGCGAGATCGTAGAGAG 811

RESULT 5
 JS-09-938-842a-64
 ; Sequence 64, Application US/09938842A
 ; Patent No. US20020160378a1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 64
 ; LENGTH: 2451
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842a-64

Query Match 22.0%; Score 28.4; DB 10; Length 2451;
 Best Local Similarity 53.6%; Pred. No. 3.2; Mismatches 51; Indels 0; Gaps 0;
 Matches 59; Conservative 0;

15 TAGCATTACTTGAGCATTACTGAGCAGCAAGACCCCGCAGATGCGGGCTCTT 74
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 791 TGGCTCTCTGCAAGAGATGCTGTTTACAAAGCTCTTACCGACTTTTGGAGGCTTG 850
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 75 TTGTTGAGTGTGAGCAGTGTGCTGCAACCGATTTATTCGAGCTAGT 124
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 851 TAGCTGATGTGTGCTGCTGCCATTGATCAGGCTGTTCATGATGAGTATGAT 900

RESULT 6
 US-10-199-672-591/c

; Sequence 591, Application US/10199672
 ; Publication No. US20030148442A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C1
 ; CURRENT APPLICATION NUMBER: US/10/199,672
 ; CURRENT FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: US/10/052,586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Remaining Prior Application data removed - See file wrapper or PAM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 591
 ; LENGTH: 2037
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-199-672-591

Query Match 21.6%; Score 27.8; DB 12; Length 2037;
 Best Local Similarity 57.5%; Pred. No. 5.1; Mismatches 37; Indels 0; Gaps 0;
 Matches 50; Conservative 0;

42 ACAAGACCCCGCAGAGATGCGGGCTTTTGTGTGCTGCTGACGTGTGTC 101
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1335 AAAAGACCATCATCTACATGTCAGGCTCATATATCTGTTGCTGACTGTGTTCC 1276
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 102 AACCGTATTTCCGAGCTAGTCAAGC 128
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1275 CTGTTGCTATCTGAGACTAATGATC 1249

RESULT 7
 US-10-187-749-591/c
 ; Sequence 591, Application US/10187749
 ; Publication No. US2003015036A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria

APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/187,749
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US/10/052,586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Remainder of SEQ ID NOS: 612
SEQ ID NO 591
LENGTH: 2037
TYPE: DNA
ORGANISM: Homo Sapien
S-10-187-749-591

Query Match 21.6%; Score 27.8; DB 12; Length 2037;
Best Local Similarity 57.5%; Pred. No. 5.1;
Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Y 42 ACAAGACCCGAGAGATGTCGGGCTTTTGTGTGTCGTGACGTGTC 101
1335 AAAAGACCATCATCTATGTCAGGCTCATTATCTGTCGACGTGTC 1276

Y 102 AACGTAATATCCGAGTATGTCAGC 128
1275 CTGTTGCTATCTGCGACTATATGCAATC 1249

b

ESULT 8
S-10-194-457-591/C
Sequence 591, Application US/10194457
Publication No. US20030153037A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C296
CURRENT APPLICATION NUMBER: US/10/194,457
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 591
LENGTH: 2037
TYPE: DNA
ORGANISM: Homo Sapien
US-10-194-457-591

Query Match 21.6%; Score 27.8; DB 12; Length 2037;
Best Local Similarity 57.5%; Pred. No. 5.1;
Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

OY 42 ACAAGACCCGAGAGATGTCGGGCTTTTGTGTGTCGTGACGTGTC 101
DB 1335 AAAAGACCATCATCTATGTCAGGCTCATTATCTGTCGACGTGTC 1276

OY 102 AACGTAATATCCGAGTATGTCAGC 128
DB 1275 CTGTTGCTATCTGCGACTATATGCAATC 1249

RESULT 9
US-10-052-586-591/C
Sequence 591, Application US/10052586
Publication No. US20020127584A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083559
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/084366
PRIOR FILING DATE:	1998-05-05
PRIOR APPLICATION NUMBER:	60/084414
PRIOR FILING DATE:	1998-05-06
PRIOR APPLICATION NUMBER:	60/084659
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084640
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084643
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/085573
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085579
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085580
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085582
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085700
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/086023
PRIOR FILING DATE:	1998-05-18
PRIOR APPLICATION NUMBER:	60/086392
PRIOR FILING DATE:	1998-05-22
PRIOR APPLICATION NUMBER:	60/086486
PRIOR FILING DATE:	1998-05-22
PRIOR APPLICATION NUMBER:	60/087098
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/087208
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/087609
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087759
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087827
PRIOR FILING DATE:	1998-06-03
PRIOR APPLICATION NUMBER:	60/088025
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088028
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088029
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088033
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088167
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088202
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088212
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088217
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088326
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088555
PRIOR FILING DATE:	1998-06-09
PRIOR APPLICATION NUMBER:	60/088722
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088738
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088740
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088811
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088824
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088825
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088826
PRIOR FILING DATE:	1998-06-10

ORGANISM: Homo Sapien

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 18:46:38 ; Search time 20.7296 Seconds
(without alignments)
2746.715 Million cell updates/sec

Title: US-09-816-391A-1_COPY_472_600

Perfect score: 129
Sequence: 1 tgaaccttcgcctcgtacgca.....tattccgactagttacgcy 129

Scoring table:
IDENTITY_NMC
Gapop 10.0 , Gapext 1.0

Searched: 569978 segs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCBUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28.6	22.2	1146	US-09-252-991A-2602	Sequence 2602, Ap
2	28.6	22.2	2184	US-09-252-991A-2241	Sequence 2241, Ap
3	28.6	22.2	2868	US-09-252-991A-2311	Sequence 2311, Ap
4	28.4	22.0	936	US-08-602-359A-31	Sequence 31, Appl
5	26.4	20.5	14707	US-09-312-762A-3	Sequence 3, Appl
6	26.2	20.3	907	US-08-672-850-7	Sequence 7, Appl
7	26.2	20.3	907	US-08-672-850-11	Sequence 11, Appl
8	26.2	20.3	907	US-09-565-177A-7	Sequence 7, Appl
9	26.2	20.3	907	US-09-565-177A-11	Sequence 11, Appl
10	26.2	20.3	1001	US-08-672-850-10	Sequence 10, Appl
11	26.2	20.3	1001	US-09-565-177A-10	Sequence 10, Appl
12	26.2	20.2	1074	US-08-934-901-7	Sequence 7, Appl
13	26.2	20.2	43280	US-08-804-227C-1	Sequence 1, Appl
14	25.8	20.0	1158	US-09-198-092-1	Sequence 1, Appl
15	25.8	20.0	2262	US-08-674-887A-5	Sequence 5, Appl
16	25.8	20.0	2262	US-08-951-844-5	Sequence 5, Appl
17	25.8	20.0	2262	US-09-412-347-5	Sequence 5, Appl
18	25.6	19.8	271	US-09-313-284A-1215	Sequence 1215, Ap
19	25.4	19.7	1586	US-08-461-244-1	Sequence 1, Appl
20	25.4	19.7	1953	US-09-016-434-1096	Sequence 1096, Ap
21	25.4	19.7	3302	US-09-221-017B-174	Sequence 174, App
22	25.2	19.5	50341	US-08-247-901C-1	Sequence 1, Appl
23	25.2	19.5	50341	US-09-075-904-1	Sequence 1, Appl
24	25.2	19.5	52297	US-08-426-436-1	Sequence 1, Appl
25	25.2	19.5	52297	US-08-705-357-1	Sequence 1, Appl
26	25.2	19.4	3613	US-09-634-238-120	Sequence 120, App
27	25.2	19.4	5798	US-08-483-101-1	Sequence 1, Appl

28	24.8	19.2	799	1	US-08-173-510B-100	Sequence 100, App
29	24.8	19.2	799	1	US-08-458-218-98	Sequence 98, Appl
30	24.8	19.2	799	2	US-08-450-497-100	Sequence 100, App
31	24.8	19.2	942	4	US-09-134-001C-2784	Sequence 2784, App
32	24.8	19.2	4067	4	US-08-894-454-164	Sequence 164, App
33	24.6	19.1	612	4	US-09-252-991A-2454	Sequence 2454, App
34	24.6	19.1	678	4	US-09-252-991A-2221	Sequence 2221, App
35	24.6	19.1	753	4	US-09-252-991A-2382	Sequence 2382, App
36	24.6	19.1	2814	4	US-09-252-991A-2537	Sequence 2537, App
37	24.6	19.1	4670	4	US-09-700-971-2	Sequence 5148, App
38	24.4	18.9	801	4	US-09-252-991A-5148	Sequence 5148, App
39	24.4	18.9	1269	4	US-09-252-991A-5037	Sequence 5037, App
40	24.4	18.9	2031	4	US-09-252-991A-5180	Sequence 5180, App
41	24.4	18.9	1830121	4	US-09-557-884-1	Sequence 1, Appl
42	24.4	18.9	1830121	4	US-09-643-990A-1	Sequence 1, Appl
43	24.2	18.8	639	4	US-09-252-991A-2342	Sequence 2342, App
44	24.2	18.8	1047	4	US-09-252-991A-11024	Sequence 11024, A
45	24.2	18.8	1092	4	US-09-252-991A-11235	Sequence 11235, A

ALIGNMENTS

```
RESULT 1
US-09-252-991A-2602/c
Sequence 2602, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2602
LENGTH: 1146
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2602

Query Match          22.2%; Score 28.6; DB 4; Length 1146;
Best Local Similarity 57.1%; Pred. No. 0.61;
Matches 52; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 39 ACGACAAAGACCCCGACGAGATGCTGCGGCTCTTTGTGTGCTGCTGACGTGTG 98
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 906 ACGATCAAGACCCGCGGCGGAGCTGCGGTATCTCTGTGATGTTCCCTGCGCTGAG 847

QY 99 TCCAACCGTATTTATCCGCGACTGATTCAGCG 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 846 TTGAGCTGCGGCAAGCTTCACAGGTGCGG 816

RESULT 2
US-09-252-991A-2241
Sequence 2241, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
```


STREET: 4425 EXECUTIVE SQUARE, STE 1400

APPLICATION NUMBER: 09/026,898

FILING DATE: 20 FEB 1998
ATTORNEY/AGENT INFORMATION:
NAME: Filedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 916/10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 14707
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-312-762A-3

Query Match 20.5%; Score 26.4; DB 4; Length 14707;
Best Local Similarity 54.0%; Pred. No. 11;
Matches 54; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Oy 7 CTCGCTGAGCGATTACTTGACGACATTAAGACACCAAGCCGAGATGGTCG 66
Db 5137 TCTTGCTCGGTGATTTTGGAGGCGCTGAGTCTGAGAACTCGTGAATGTCGA 5078

Oy 67 GGGCTTTTGTGTGGTGGCTGTGACGCTGTTCACCG 106
Db 5077 GCTTGTGGGCTCGACACAAAGATGGGTCCACAGC 5038

RESULT 6
US-08-672-850-7/C
Sequence 7, Application US/08672850
Patent No. 6140117
GENERAL INFORMATION:
APPLICANT: Albrandt, Jeffrey
APPLICANT: Arai, Toshiyuki
TITLE OF INVENTION: NINJURIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,850
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 907 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-672-850-7

Query Match 20.3%; Score 26.2; DB 3; Length 907;
Best Local Similarity 58.2%; Pred. No. 4.2;

Matches 46; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Oy 11 CTCGTACGATTACTTGACGACATTAAGACACCAAGCCGAGATGGTGGGT 70
Db 434 CCCGAGCGCTGATGAAACATTGATGACACAGTGAGAGAACCAAGATGGTGGTGC 375

Oy 71 CTTTGTGTGGTGGTGGT 89
Db 374 GTTGTGAGCTGTTGAGT 356

RESULT 7
US-08-672-850-11/C
Sequence 11, Application US/08672850
Patent No. 6140117
GENERAL INFORMATION:
APPLICANT: Albrandt, Jeffrey
APPLICANT: Arai, Toshiyuki
TITLE OF INVENTION: NINJURIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,850
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 907 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-672-850-11

Query Match 20.3%; Score 26.2; DB 3; Length 907;
Best Local Similarity 58.2%; Pred. No. 4.2;
Matches 46; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Oy 11 CTCGTACGATTACTTGACGACATTAAGACACCAAGCCGAGATGGTGGGT 70
Db 434 CCCGAGCGCTGATGAAACATTGATGACACAGTGAGAGAACCAAGATGGTGGTGC 375

Oy 71 CTTTGTGTGGTGGTGGT 89
Db 374 GTTGTGAGCTGTTGAGT 356

RESULT 8
US-09-565-177A-7/C
Sequence 7, Application US/09565177A
Patent No. 6559288
GENERAL INFORMATION:
APPLICANT: Albrandt, Jeffrey
APPLICANT: Arai, Toshiyuki
TITLE OF INVENTION: NINJURIN

RESULT 12
US-09-934-901-7/c
Sequence 7, Application US/09934901
Patent No. 655353
GENERAL INFORMATION:
APPLICANT: Koffas, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: No. 655353ton, Kelley C.
APPLICANT: Ye, Rick
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: C1619 US NA
CURRENT APPLICATION NUMBER: US/09/934,901
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,906
PRIOR FILING DATE: September 1, 2000
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
LENGTH: 1074
TYPE: DNA
ORGANISM: METHYLOMONAS SP.
US-09-934-901-7

Query Match 20.2%; Score 26; DB 4; Length 1074;
Best Local Similarity 62.1%; Pred. No. 5.3;
Matches 41; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 37 TGACGACAAAGACCCGACGAGATGCTTTTGTGTGTGCTGTGACGTGT 96
DB 670 TGCCGAAAGACCCGACGAGATGCTTTTGTGTGTGCTGTGACGTGT 611
OY 97 TGTCCA 102
DB 610 AAGCCA 605

RESULT 13
US-08-804-227C-1/c
Sequence 1, Application US/08804227C
Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: Dehoff, Bradley S.
APPLICANT: Kumbloss, Stuart A.
APPLICANT: Kosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 43280 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 816..14234
FEATURE:
NAME/KEY: CDS
LOCATION: 14351..19945
FEATURE:
NAME/KEY: CDS
LOCATION: 20010..31199
FEATURE:
NAME/KEY: CDS
LOCATION: 31232..36067
FEATURE:
NAME/KEY: CDS
LOCATION: 36249..41774
US-08-804-227C-1

Query Match 20.2%; Score 26; DB 2; Length 43280;
Best Local Similarity 55.6%; Pred. No. 24;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 38 GAGGACAAAGACCCGACGAGATGCTTTTGTGTGTGCTGTGACGTGT 97
DB 13262 GACCGGACAAAGACCCGACGAGATGCTTTTGTGTGTGCTGTGACGTGT 13203
OY 98 GTCAACCGGATTTATTCGCGACTAGTTTCAG 127
DB 13202 CGCTTCGCGGACGATGACGTACCGATCCG 13173

RESULT 14
US-09-198-092-1/c
Sequence 1, Application US/09198092A
Patent No. 6214575
GENERAL INFORMATION:
APPLICANT: Yano, Masamitsu
APPLICANT: Omura, Mitsuo
APPLICANT: Ikoma, Yoshiro
TITLE OF INVENTION: BETA-CAROTENE HYDROXYLASE GENE
FILE REFERENCE: 07898/033001
CURRENT APPLICATION NUMBER: US/09/198,092A
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: JP97/331936
EARLIER FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1158
TYPE: DNA
ORGANISM: Citrus unshiu
FEATURE:
NAME/KEY: CDS
LOCATION: (87)..(1019)
US-09-198-092-1

Query Match 20.0%; Score 25.8; DB 3; Length 1158;
Best Local Similarity 63.9%; Pred. No. 6.5;
Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 37 TGACGACAAAGACCCGACGAGATGCTTTTGTGTGTGCTGTGACGTGT 96
DB 111 TGCGGCGCAATAGCCGACCGCATGCTGGGGTTTGTGTGTACGAGCTTTG 52
OY 97 T 97
DB 51 T 51

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 18:56:32 ; Search time 73.798 Seconds
(without alignments)
5849.036 Million cell updates/sec

Title: US-09-816-391A-1_COPY_1_192

Perfect score: 192
Sequence: 1 gcgcggcgcgcgccatga.....tgaccacagaagatgcttc 192

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCr_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCrTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09C_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	192	100.0	600	US-09-816-391A-1	Sequence 1, Appl1
2	33.2	17.3	824	US-10-027-632-167810	Sequence 167810,
3	32.4	16.9	484	US-10-027-632-6585	Sequence 6585, Ap
4	31.2	16.2	18372	US-09-764-891-8869	Sequence 8869, Ap
5	30.6	15.9	1099	US-10-027-632-10536	Sequence 10536, A
6	30.2	15.7	515	US-09-864-761-16206	Sequence 16206, A
7	30	15.6	639	US-10-027-632-18596	Sequence 18596,
8	29.8	15.5	501	US-10-027-632-270844	Sequence 270844,
9	29.6	15.4	453	US-10-027-632-266872	Sequence 266872,
10	29.4	15.3	487	US-09-918-995-12674	Sequence 12674, A
11	29.4	15.3	614	US-10-027-632-221811	Sequence 221811,
12	29.4	15.3	514	US-10-027-632-221811	Sequence 221811,
13	29.2	15.2	607	US-09-796-692-4795	Sequence 4795, Ap
14	29.2	15.2	507	US-10-040-862-4795	Sequence 4795, Ap
15	29.2	15.2	1712	US-10-027-632-97328	Sequence 97328, A
16	29.2	15.2	1712	US-10-027-632-97329	Sequence 97329, A

17	29.2	15.2	2190	14	US-10-217-371-5	Sequence 5, Appl1
18	29.2	15.2	2250	14	US-10-217-371-13	Sequence 13, Appl1
19	29.2	15.2	2253	14	US-10-217-371-3	Sequence 3, Appl1
20	29.2	15.2	2274	14	US-10-217-371-9	Sequence 9, Appl1
21	29.2	15.2	2313	14	US-10-217-371-11	Sequence 11, Appl1
22	29.2	15.2	2337	14	US-10-217-371-7	Sequence 7, Appl1
23	29.2	15.2	2508	14	US-10-176-847-1	Sequence 1, Appl1
24	29.2	15.2	2937	14	US-10-176-847-45	Sequence 45, Appl1
25	29.2	15.2	3077	12	US-10-301-822-150	Sequence 150, App
26	29.2	15.2	3077	14	US-10-171-311-179	Sequence 179, App
27	29.2	15.2	3202	9	US-09-925-301-471	Sequence 471, App
28	29.2	15.2	3213	12	US-10-301-822-148	Sequence 148, App
29	29.2	15.2	3213	12	US-10-304-752-32	Sequence 32, Appl1
30	29.2	15.2	3213	14	US-10-171-311-177	Sequence 177, App
31	29.2	15.2	3213	14	US-10-177-293-341	Sequence 341, App
32	29.2	15.2	3681	14	US-10-198-846-981	Sequence 9861, Ap
33	29.2	15.2	6465	10	US-09-954-456-193	Sequence 193, App
34	29	15.1	1444	14	US-10-106-698-1319	Sequence 1319, Ap
35	29	15.1	1830121	14	US-10-329-960-1	Sequence 1, Appl1
36	28.8	15.0	413	10	US-09-867-701-2315	Sequence 2315, Ap
37	28.8	15.0	419	10	US-09-783-590-663	Sequence 663, App
38	28.8	15.0	611	13	US-10-027-632-209927	Sequence 209927,
39	28.8	15.0	611	13	US-10-027-632-209928	Sequence 209928,
40	28.8	15.0	611	13	US-10-027-632-209929	Sequence 209929,
41	28.8	15.0	611	13	US-10-027-632-209930	Sequence 209930,
42	28.8	15.0	835	13	US-10-027-632-160356	Sequence 160356,
43	28.4	14.8	345	10	US-09-974-300-3770	Sequence 3770, Ap
44	28.4	14.8	75899	9	US-09-854-883-243	Sequence 243, App
45	28.2	14.7	279	12	US-10-238-075-413	Sequence 413, App

ALIGNMENTS

RESULT 1

US-09-816-391A-1

Sequence 1, Application US/09816391A

Patent No. US20020054865A1

GENERAL INFORMATION:

APPLICANT: FUJIMORI, Minoru

APPLICANT: TANIGUCHI, Shunichiro

APPLICANT: AMANO, Jun

APPLICANT: YAZAWA, Kazuyuki

APPLICANT: KANO, Yasunobu

APPLICANT: NAKAMURA, Toshiyuki

APPLICANT: SASAKI, Takayuki

TITLE OF INVENTION: Anaerobic bacterium as a drug for cancer gene therapy

FILE REFERENCE: 2001-WMC/01736

CURRENT APPLICATION NUMBER: US/09/816,391A

CURRENT FILING DATE: 2001-03-26

PRIOR APPLICATION NUMBER: JP 00/287688

PRIOR FILING DATE: 2000-09-21

NUMBER OF SEQ ID NOS: 3

SEQ ID NO 1

LENGTH: 600

TYPE: DNA

ORGANISM: Bifidobacterium longum

FEATURE:

NAME/KEY: CDS

LOCATION: (193)..(471)

US-09-816-391A-1

Query Match 100.0%; Score 192; DB 9; Length 600;

Best Local Similarity 100.0%; Pred. No. 7.2e-55;

Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGTGGCGCGCGCGCGCAAGAGTGGCTTGACAGCATATCTTGTCATTCGCTATTT 60

1 GCTGGCGCGCGCGCGCAAGAGTGGCTTGACAGCATATCTTGTCATTCGCTATTT 60

61 TCAATACCTTGGGGGAATAGATGGAACCCCTATATAACCGGGGTTTCGCAAGAAC 120

61 TCAATACCTTGGGGGAATAGATGGAACCCCTATATAACCGGGGTTTCGCAAGAAC 120

QY 121 AAGCGTAGTATCATGATGACATGACATGACAAAGTCGTCGCTGACCCCA 180
 |||
 DB 121 AAGCGTAGTATCATGATGACATGACATGACAAAGTCGTCGCTGACCCCA 180
 |||
 QY 181 GAAGATGCTTT 192
 |||
 DB 181 GAAGATGCTTT 192

RESULT 2
 US-10-027-632-167810/c
 ; Sequence 167810, Application US/10027632
 ; GENERAL INFORMATION:

APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: 108827.129
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 167810
 ; LENGTH: 824
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-167810

Query Match 17.3%; Score 33.2; DB 13; Length 824;
 Best Local Similarity 59.6%; Pred. No. 0.62;
 Matches 56; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 76 AATAGATGTGAAACCCCTATATAAAGCGGGTTTCGAGAAACATGCGCTAGTTCAT 135
 |||
 DB 384 AATATAATAGAAACCAAGAGTAAGCAATATATAAAGGTTGAACATGATCTA 325
 |||
 QY 136 TGATGACATGACTAGCTAGCAAAAGTGCTGTC 169
 |||
 DB 324 TGATGACAAAGTCTATAGCAAGGTTGTATTC 291

RESULT 3
 US-10-027-632-6585

; Sequence 6585, Application US/10027632
 ; GENERAL INFORMATION:

APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: 108827.129
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6585
 ; LENGTH: 484
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-6585

Query Match 16.9%; Score 32.4; DB 13; Length 484;
 Best Local Similarity 60.7%; Pred. No. 0.89;
 Matches 51; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY 36 ATAATCTGTCTGATCGCTATATTTCAATACCTTCGGGAAATAGATGAAACCTT 95
 |||
 DB 130 AGAATATCTTTTCACACCTACTGTATATCCCTCGGCTAATAGCATGACATATA 189
 |||
 QY 96 ATAAACGCGGCTTTTCGACAAA 119
 |||
 DB 190 ATGAATACTTTTCTTGAGAAA 213

RESULT 4
 US-09-764-891-8869/c

; Sequence 8869, Application US/09764891
 ; Publication No. US20030077808A1
 ; GENERAL INFORMATION:

APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC006
 ; CURRENT APPLICATION NUMBER: US/09/764,891
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 10231
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8869
 ; LENGTH: 18272
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-891-8869

Query Match 16.2%; Score 31.2; DB 11; Length 18272;
 Best Local Similarity 60.7%; Pred. No. 13;
 Matches 51; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 71 CGGGGAATAGATGTGAACCCCTATATAAAGCGGGTTTCGAGAAACATGCGCTAGT 130
 |||
 DB 17088 CGAGGAGAGAGAGATGAAGAAAGGACAGAGATGTGAGAGTGTGACGACAGACGTGGGCGAGG 17029
 |||
 QY 131 ATCATTGATGACACATGACTAA 154
 |||
 DB 17028 AACACCATGAGAACAGGACTCA 17005

RESULT 5
 US-10-027-632-10536/c

; Sequence 10536, Application US/10027632
 ; GENERAL INFORMATION:

APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: 108827.129
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20

;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 10536
;; LENGTH: 1099
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-10536

Query Match 15.9%; Score 30.6; DB 13; Length 1099;
Best Local Similarity 50.3%; Pred. No. 5.4; Mismatches 0; Gaps 0;
Matches 75; Conservative 0; Indels 74; Indels 0; Gaps 0;

QY 35 CATATCTGTGTCGATTCGTATTTTCATACCTTCGGGGAATAGATGAAACCTT 94
DB 202 CATGTTTATTTAAATGAGACTTTTCAAAACCTTGTTGTTTATTTACCAACATA 143
QY 95 TTTAAACGGGGTTTCCGACGAAACATGCGCTAGATATCTTGTATGACATGAGCTAA 154
DB 142 AATTGAAACGACCTTACGACATTTAAGATGACGATTTAATTAACATGAAAT 83
QY 155 GCAAAAGTCCTGTCCTCCCTGACCCAGAA 183
DB 82 TTTAAATGTTTGCACATTTACCCATGTA 54

RESULT 6
US-09-864-761-16206
;; Sequence 16206, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: Aecm1ca-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 16206
;; LENGTH: 515
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC00062.1
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
US-09-864-761-16206

Query Match 15.7%; Score 30.2; DB 9; Length 515;
Best Local Similarity 49.7%; Pred. No. 5.1; Mismatches 0; Gaps 0;
Matches 77; Conservative 0; Indels 78; Indels 0; Gaps 0;

QY 13 GCCATGAAGTGGCTTGACACATATCTGTGATTCGTCCTATTTTCATACCTTG 72
DB 253 GCCCTTAAATATGACGATGATATTTATCTTTAGTGAATGAGATTTTAAACCTTAA 312
QY 73 GGAATATAGATGTGAACACCTTATTAACGCGGTTTCCGACGAAACATGCGCTAGAT 132
DB 313 TAGAAGTATGATGATTAACATTCACATTAATGTTTATGATGATGATGATGATGAT 372
QY 133 CATGATGACACATGACATGACATGACAAAGTCTTG 167
DB 373 GTTTACTGCTCTTAAACTTTTGAACCTGCTG 407

RESULT 7
US-10-027-632-185956/C
;; Sequence 185956, Application US/10027632
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; PRIOR FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 185956
;; LENGTH: 639
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(639)

OTHER INFORMATION: n - A,T,C or G
US-10-027-632-185956

Query Match 15.6%; Score 30; DB 13; Length 639;
Best Local Similarity 59.3%; Pred. No. 6.6;
Matches 51; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

OY 16 CAGCAATGGCTGACACAGCATATCTGTGATGCTCATTTTCAATACCTTCGGGG 75
DB 629 CAGCACTGGCTGACATGATGATGATTTTAAATTTCTGACGTTAAACATTTTATA 570
OY 76 AAATGATGTGAAACCTTTAAAA 101
DB 569 TAAGCATTTTGAACACTTAAAAA 544

RESULT 8
US-10-027-632-270844/c
Sequence 270844, Application US/10027632
GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIORITY FILING DATE: 2002-04-30
PRIORITY APPLICATION NUMBER: US 60/218,006
PRIORITY FILING DATE: 2000-07-12
PRIORITY APPLICATION NUMBER: US 60/199,676
PRIORITY FILING DATE: 2000-04-20
PRIORITY APPLICATION NUMBER: US 60/193,483
PRIORITY FILING DATE: 2000-03-29
PRIORITY APPLICATION NUMBER: US 60/185,218
PRIORITY FILING DATE: 2000-02-24
PRIORITY APPLICATION NUMBER: US 60/167,363
PRIORITY FILING DATE: 1999-11-23
PRIORITY APPLICATION NUMBER: US 60/156,358
PRIORITY FILING DATE: 1999-09-28
PRIORITY APPLICATION NUMBER: US 60/146,002
PRIORITY FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 270844
LENGTH: 501
TYPE: DNA
ORGANISM: Human
US-10-027-632-270844

Query Match 15.5%; Score 29.8; DB 13; Length 501;
Best Local Similarity 54.0%; Pred. No. 6.9;
Matches 61; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

OY 1 GCTGGGGCGGGCGGCATGAGTGGCTTGACACATATCTGTGATGCTCATTTT 60
DB 484 GCTTGTGGCGGGCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
OY 61 TCAATACCTGGGGGGAATAGATGGAACCCCTTATTTAAAAAGGGGGTTTCG 113
DB 424 ATTAACCATCTGGAACCTCTGGGCACTGTCTTATTAATTAAGTCAACATTG 372

RESULT 9
US-10-027-632-266872/c
Sequence 266872, Application US/10027632
GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIORITY FILING DATE: 2002-04-30
PRIORITY APPLICATION NUMBER: US 60/218,006
PRIORITY FILING DATE: 2000-07-12

PRIORITY APPLICATION NUMBER: US 60/198,676
PRIORITY FILING DATE: 2000-04-20
PRIORITY APPLICATION NUMBER: US 60/193,483
PRIORITY FILING DATE: 2000-03-29
PRIORITY APPLICATION NUMBER: US 60/185,218
PRIORITY FILING DATE: 2000-02-24
PRIORITY APPLICATION NUMBER: US 60/167,363
PRIORITY FILING DATE: 1999-11-23
PRIORITY APPLICATION NUMBER: US 60/156,358
PRIORITY FILING DATE: 1999-09-28
PRIORITY APPLICATION NUMBER: US 60/146,002
PRIORITY FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 266872
LENGTH: 453
TYPE: DNA
ORGANISM: Human
US-10-027-632-266872

Query Match 15.4%; Score 29.6; DB 13; Length 453;
Best Local Similarity 61.8%; Pred. No. 7.7;
Matches 47; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

OY 16 CAGCACTGGCTGACACAGCATATCTGTGATGCTCATTTTCAATACCTTCGGG 75
DB 435 CAGTATTAATCTTTAACTGCAAAACCTCATCTGCTGTTTAAAGACCTTATGA 376
OY 76 AAATGATGTGAAAC 91
DB 375 AAAGATACAGGACAC 360

RESULT 10
US-09-918-995-12674
Sequence 12674, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
PRIORITY FILING DATE: 2001-07-30
PRIORITY APPLICATION NUMBER: US/09/235,076
PRIORITY FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12674
LENGTH: 487
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(487)
OTHER INFORMATION: n - A,T,C or G
US-09-918-995-12674

Query Match 15.3%; Score 29.4; DB 11; Length 487;
Best Local Similarity 55.3%; Pred. No. 9.3;
Matches 57; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

OY 20 AAGTGGCTTGACAGCATATCTGTGATGCTCATTTTCAATACCTTCGGGAAAT 79
DB 251 AAGCAATTTGTTAGTTAACTTCCCTGATGATGATTTTAAAAAACACAGTGAAAA 310
OY 80 AGATGTGAAAAACCTTATTAACCGGGGTTTTCGACAAACAT 122
DB 311 AAATACACAGCACTAGATGATGATTTTTCGACAACTACTT 353

RESULT 11
US-10-027-632-221811/c

```
; Sequence 221811, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221811
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-221811

Query Match      15.3%; Score 29.4; DB 13; Length 614;
Best Local Similarity 52.0%; Pred. No. 10;
Matches 66; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

OY      55 CATTTCATACCTCGGGGAATGATGTGAAACCCCTATATAACGGGGTTTCGC 114
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      291 CAGTCTTTTCACTCTTAAATAATATGTCAAAATCTGTTGAAAAAGAAATATATGC 232
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      115 AGAAACATGCGGTAGTATCTTGTATGACACATGACATGACAAAGTGTGCCCCCTG 174
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      231 ATAAATATAAAACATACAAACATATATAAATGAAATGTTAAATGCTTCTCTCTG 172
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      175 ACCCAAG 181
      | ||
Db      171 TCTTCAG 165
```

```
; SEQ ID NO 221812
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-221812

Query Match      15.3%; Score 29.4; DB 13; Length 614;
Best Local Similarity 52.0%; Pred. No. 10;
Matches 66; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

OY      55 CATTTCATACCTCGGGGAATGATGTGAAACCCCTATATAACGGGGTTTCGC 114
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      291 CAGTCTTTTCACTCTTAAATAATATGTCAAAATCTGTTGAAAAAGAAATATATGC 232
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      115 AGAAACATGCGGTAGTATCTTGTATGACACATGACATGACAAAGTGTGCCCCCTG 174
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      231 ATAAATATAAAACATACAAACATATATAAATGAAATGTTAAATGCTTCTCTCTG 172
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      175 ACCCAAG 181
      | ||
Db      171 TCTTCAG 165

RESULT 13
US-09-796-692-4795
; Sequence 4795, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4795
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-796-692-4795

Query Match      15.2%; Score 29.2; DB 10; Length 507;
Best Local Similarity 59.8%; Pred. No. 11;
Matches 49; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY      89 ACCCTATAAACGGGGTTTCGACGAAACATGCGCTAGTATCATGATGACACATG 148
```

b 339 AACCATATCTTAATGGGGTGTCTCATCTTAATGTGCTCAATCATTCATCGGAACGAG 398
y 149 GACTAAGCAAAAGTCTGTCC 170
b 399 ATTGCAACAATAGTGTGTCC 420

ESULT 14

S-10-040-862-4795.
Sequence 4795, Application US/10040862
Publication No. US20030078396A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

FILE REFERENCE: 014058-013520US

CURRENT FILING DATE: 2001-11-06

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,779

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,999

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: US 60/202,084

PRIOR FILING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: US 60/206,201

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: US 60/218,950

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 60/222,903

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: US 60/223,416

PRIOR FILING DATE: 2000-08-04

PRIOR APPLICATION NUMBER: US 60/223,378

PRIOR FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: US 09/796,692

PRIOR FILING DATE: 2001-03-01

NUMBER OF SEQ ID NOS: 10467

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4795

LENGTH: 507

TYPE: DNA

ORGANISM: Homo sapiens

S-10-040-862-4795

Query Match 15.2%; Score 29.2; DB 14; Length 507;
Best Local Similarity 59.8%; Pred. No. 11;
Matches 49; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

y 89 AACCTTATTAACCGGGTTTTCAGAAACATCGCTAGATCATTCATGATGACAACATG 148
b 339 AACCTTATCTTAATGGGGTGTCTCATCTTAATGTGCTCAATCATTCATCGGAACGAG 398
y 149 GACTAAGCAAAAGTCTGTCC 170
b 399 ATTGCAACAATAGTGTGTCC 420

ESULT 15
S-10-027-632-97328
Sequence 97328, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97328
LENGTH: 1712
TYPE: DNA
ORGANISM: Human
S-10-027-632-97328

Query Match 15.2%; Score 29.2; DB 13; Length 1712;
Best Local Similarity 48.8%; Pred. No. 20;
Matches 79; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

y 20 AAGTGGCTTGACAAACATATCTGTCTGATTCGCTATTTTCAATACCTTCGGGGAAT 79
b 1490 AAGTGGCTCTTAAGGATTAATCTAGCTACAGTGTCTAGAAATTTCTTGATGAAGTT 1549
y 80 AGATGTGAACCCCTTAAACGCGGTTTTCAGAAACATCGCTAGATCATTCATGAT 139
b 1550 AGAAGTGAAGTCTTACACAGATTAATCTTCAGAGAGGACATTTGTAAAGCATTTAT 1609
y 140 GACAACATGACTAAGCAAAAGTCTGTCTCCCTGACCCAG 181
b 1610 TACACTGGTGGAGGAGCAATCTGCTCTGTTCAAG 1651

Search completed: August 25, 2003, 22:04:22
Job time : 76.798 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 18:48:22 ; Search time 1513.9 Seconds

Title:	US-09-816-391A-1_COPY_1_192
Perfect score:	192
Sequence:	1 gctggcgcgcgcgccatga.....tgaccagaagatgcttt 192

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32997241 seqs, 16383922548 residues

Total number of hits satisfying chosen parameters: 65994482

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

Database :

```

1: pendInLn_Patients_NA_Main: *
2: /cgn2_6/p/codata/1/pna/PCRTUS_COMB.seq.*
3: /cgn2_6/p/codata/1/pna/PCRTUS_COMB.seq.0ld.*
4: /cgn2_6/p/codata/1/pna/US06_COMB.seq.*
5: /cgn2_6/p/codata/1/pna/US07_COMB.seq.*
6: /cgn2_6/p/codata/1/pna/US08_COMB.seq.*
7: /cgn2_6/p/codata/1/pna/US081_COMB.seq.*
8: /cgn2_6/p/codata/1/pna/US082_COMB.seq.*
9: /cgn2_6/p/codata/1/pna/US083_COMB.seq.*
10: /cgn2_6/p/codata/1/pna/US084_COMB.seq.*
11: /cgn2_6/p/codata/1/pna/US085_COMB.seq.*
12: /cgn2_6/p/codata/1/pna/US086_COMB.seq.*
13: /cgn2_6/p/codata/1/pna/US087_COMB.seq.*
14: /cgn2_6/p/codata/1/pna/US088_COMB.seq.*
15: /cgn2_6/p/codata/1/pna/US089_COMB.seq.*
16: /cgn2_6/p/codata/1/pna/US090_COMB.seq.*
17: /cgn2_6/p/codata/1/pna/US091_COMB.seq.*
18: /cgn2_6/p/codata/1/pna/US092a_COMB.seq.*
19: /cgn2_6/p/codata/1/pna/US092b_COMB.seq.*
20: /cgn2_6/p/codata/1/pna/US093a_COMB.seq.*
21: /cgn2_6/p/codata/1/pna/US093b_COMB.seq.*
22: /cgn2_6/p/codata/1/pna/US094_COMB.seq.*
23: /cgn2_6/p/codata/1/pna/US095a_COMB.seq.*
24: /cgn2_6/p/codata/1/pna/US095b_COMB.seq.*
25: /cgn2_6/p/codata/1/pna/US095c_COMB.seq.*
26: /cgn2_6/p/codata/1/pna/US096a_COMB.seq.*
27: /cgn2_6/p/codata/1/pna/US096b_COMB.seq.*
28: /cgn2_6/p/codata/1/pna/US096c_COMB.seq.*
29: /cgn2_6/p/codata/1/pna/US096d_COMB.seq.*
30: /cgn2_6/p/codata/1/pna/US096E_COMB.seq.*
31: /cgn2_6/p/codata/1/pna/US097a_COMB.seq.*
32: /cgn2_6/p/codata/1/pna/US097b_COMB.seq.*
33: /cgn2_6/p/codata/1/pna/US097c_COMB.seq.*
34: /cgn2_6/p/codata/1/pna/US098a_COMB.seq.*
35: /cgn2_6/p/codata/1/pna/US098b_COMB.seq.*
36: /cgn2_6/p/codata/1/pna/US098c_COMB.seq.*
37: /cgn2_6/p/codata/1/pna/US098d_COMB.seq.*
38: /cgn2_6/p/codata/1/pna/US099a_COMB.seq.*
39: /cgn2_6/p/codata/1/pna/US099b_COMB.seq.*
40: /cgn2_6/p/codata/1/pna/US099c_COMB.seq.*
41: /cgn2_6/p/codata/1/pna/US099d_COMB.seq.*
42: /cgn2_6/p/codata/1/pna/US099E_COMB.seq.*
43: /cgn2_6/p/codata/1/pna/US099F_COMB.seq.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	DB	ID	Description
1	192	100.0	600	34	US-09-816-391A-1	Sequence 1, Appl1
2	34.6	18.0	425	20	US-09-354-745-1867	Sequence 1867, A
3	34.6	18.0	425	25	US-09-565-306-42355	Sequence 42355, A
4	34.6	18.0	425	28	US-09-654-617-322494	Sequence 322494, A

```

c 5 34.6 18.0 425 30 US-09-684-016-322494 Sequence 322494,
6 34 17.7 180220 75 US-60-212-664-193 Sequence 193, App
7 34 17.7 685326 40 US-09-947-916-137 Sequence 137, App
8 33.4 17.4 589 27 US-09-637-890-992 Sequence 992, App
9 33.4 17.4 50000 22 US-09-513-647B-11 Sequence 11, App
c 10 33.4 17.4 2420479 40 US-09-947-911-305 Sequence 305, App
c 11 33.2 17.3 824 27 US-09-634-306B-167810 Sequence 167810,
c 12 33.2 17.3 824 27 US-10-027-632-167810 Sequence 167810,
c 13 33.2 17.3 32768 74 US-60-207-422-55 Sequence 55, App
c 14 33.2 17.3 133318 22 US-09-528-237A-20 Sequence 20, App
c 15 32.8 17.1 12360069 40 US-09-948-128-318 Sequence 318, App
c 16 32.6 17.0 278 22 US-09-513-999C-31601 Sequence 31601, App
c 17 32.6 17.0 2570 46 US-10-144-771-6009 Sequence 6009, App
c 18 32.6 17.0 2570 91 US-60-360-207-6009 Sequence 6009, App
c 19 32.4 16.9 484 27 US-09-634-306B-6585 Sequence 6585, App
c 20 32.4 16.9 484 27 US-10-027-632-6585 Sequence 6585, App
c 21 32.4 16.9 2717 26 US-09-614-150-30178 Sequence 30178, App
c 22 32.4 16.9 2717 73 US-60-191-637-29726 Sequence 29726, App
c 23 32.4 16.9 1160003 40 US-09-528-237A-921 Sequence 921, App
c 24 32.4 16.9 1160003 40 US-09-947-911-238 Sequence 238, App
c 25 32.2 16.8 525 35 US-09-834-366-9232 Sequence 9232, App
c 26 32.2 16.8 525 73 US-60-197-873-9232 Sequence 9232, App
c 27 32 16.7 495269 51 US-60-252-833-30435 Sequence 30435, App
c 28 32 16.7 495269 51 US-10-398-221-8 Sequence 8, App
c 29 32 16.7 3011308 51 US-10-398-221-2058 Sequence 2058, App
c 30 31.8 16.6 398 30 US-09-699-999-3551 Sequence 3551, App
c 31 31.8 16.6 175847 35 US-09-855-768-18 Sequence 18, App
c 32 31.8 16.6 1059516 40 US-09-947-911-86 Sequence 86, App
c 33 31.6 16.5 438 25 US-09-394-745-12555 Sequence 12555, App
c 34 31.6 16.5 438 25 US-09-565-306-32998 Sequence 32998, App
c 35 31.6 16.5 670 74 US-09-865-439A-59941 Sequence 59941, App
c 36 31.6 16.5 670 74 US-60-207-458-104101 Sequence 104101, App
c 37 31.6 16.5 1878 28 US-09-654-617-261052 Sequence 261052, App
c 38 31.6 16.5 1878 30 US-09-684-016-261052 Sequence 261052, App
c 39 31.4 16.4 384 19 US-09-304-517A-91809 Sequence 91809, App
c 40 31.4 16.4 384 20 US-09-394-745-19452 Sequence 19452, App
c 41 31.4 16.4 384 25 US-09-565-306-42940 Sequence 42940, App
c 42 31.4 16.4 384 25 US-09-985-678-91809 Sequence 91809, App
c 43 31.4 16.4 501 20 US-09-371-146A-91809 Sequence 91809, App
c 44 31.4 16.4 161812 22 US-09-528-237A-1697 Sequence 1697, App
c 45 31.2 16.2 140 28 US-09-654-617-87312 Sequence 87312, App
```

ALIGNMENTS

```

Query Match 100.0%; Score 192; DB 34; Length 600;
Best Local Similarity 100.0%; Pred. No. 4e-51;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGGGGGGGGGCCCATGATGGCTTGCAGACATATCTGTGATGCTATTTT 60
D 1 GCTGGGGGGGGGGCCCATGATGGCTTGCAGACATATCTGTGATGCTATTTT 60
QY 61 TCATACCTTCGGGGGAATATGATGTGAACCCCTATTAACCGGGTTTCGAGAAC 120
D 61 TCATACCTTCGGGGGAATATGATGTGAACCCCTATTAACCGGGTTTCGAGAAC 120
QY 121 ATCGCGTAGATATGATGATACACATGACTAGCAAAAAGTCTTCCCTGACCCAA 180
D 121 ATCGCGTAGATATGATGATACACATGACTAGCAAAAAGTCTTCCCTGACCCAA 180
QY 181 GAAGATGCTTT 192
D 181 GAAGATGCTTT 192
```

```

RESULT 1
US-09-816-391a-1
: Sequence 1, Application US/09816391A
: GENERAL INFORMATION:
: APPLICANT: FUJIMORI, Minoru
: APPLICANT: TANIGUCHI, Shunichihiro
: APPLICANT: AMANO, Jun
: APPLICANT: YAZAWA, Kazuyuki
: APPLICANT: KANO, Yasunobu
: APPLICANT: NAKAMURA, Toshiyuki
: APPLICANT: SASAKI, Takayuki
: TITLE OF INVENTION: Anaerobic bacterium as a drug for cancer gene therapy
: FILE REFERENCE: 2001-WK/01736
: CURRENT APPLICATION NUMBER: US/09/816, 391A
: PRIOR FILING DATE: 2001-03-26
: PRIOR FILING DATE: 2000-09-21
: NUMBER OF SEQ ID NOS: 3
: SEQ ID NO 1
: LENGTH: 600
: TYPE: DNA
: ORGANISM: Bifidobacterium longum
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (193)..(471)
: US-09-816-391a-1
```

```

Query Match 100.0%; Score 192; DB 34; Length 600;
Best Local Similarity 100.0%; Pred. No. 4e-51;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGGGGGGGGGCCCATGATGGCTTGCAGACATATCTGTGATGCTATTTT 60
D 1 GCTGGGGGGGGGGCCCATGATGGCTTGCAGACATATCTGTGATGCTATTTT 60
QY 61 TCATACCTTCGGGGGAATATGATGTGAACCCCTATTAACCGGGTTTCGAGAAC 120
D 61 TCATACCTTCGGGGGAATATGATGTGAACCCCTATTAACCGGGTTTCGAGAAC 120
QY 121 ATCGCGTAGATATGATGATACACATGACTAGCAAAAAGTCTTCCCTGACCCAA 180
D 121 ATCGCGTAGATATGATGATACACATGACTAGCAAAAAGTCTTCCCTGACCCAA 180
QY 181 GAAGATGCTTT 192
D 181 GAAGATGCTTT 192
```

```

RESULT 2
US-09-394-745-18867/c
: Sequence 18867, Application US/09394745
: GENERAL INFORMATION:
: APPLICANT: Fisher, Dane K.
: APPLICANT: Laligudi, Raghunath V.
: TITLE OF INVENTION: NOCLETIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WI
: FILE REFERENCE: 38-21(115454)B
: CURRENT APPLICATION NUMBER: US/09/394, 745
: CURRENT FILING DATE: 1999-09-15
: NUMBER OF SEQ ID NOS: 57264
: SEQ ID NO 18867
: LENGTH: 425
: TYPE: DNA
: ORGANISM: Zea mays
: OTHER INFORMATION: Clone ID: LIB3062-017-Q1-K1-C7
: US-09-394-745-18867

Query Match 18.0%; Score 34.6; DB 20; Length 425;
Best Local Similarity 51.6%; Pred. No. 3.6;
Matches 79; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 16 CATGAGTGGCTGACAGACATATCTGTGATGCTATTTTCAATACCTGCGG 75
D 187 CTGAATCTGACGACAGATTAATTTTCCACCAACAAATACATATATGTC 128
QY 76 AATAGATGTGAACCCCTTAATAACGCGGTTTCGAGAACATGCGCTAGTATCAT 135
D 127 AATGACGCAATTAATCATTTGAATGCTATTTACATATATCAAGACACTGTAAGT 68
QY 136 TGATGACACATGACTAGCAAAAAGTCTTGT 168
D 67 TACTGCCACAAATAGCTAAACAGAGAGGTGT 35

RESULT 3
US-09-565-306-42355/c
: Sequence 42355, Application US/09565306
: GENERAL INFORMATION:
: APPLICANT: Andersen, Scott E.
: APPLICANT: Conner, Timothy W.
: APPLICANT: Laligudi, Raghunath V.
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated wi
: FILE REFERENCE: 38-21(115459)C
: CURRENT APPLICATION NUMBER: US/09/565, 306
: CURRENT FILING DATE: 2000-05-04
: NUMBER OF SEQ ID NOS: 83523
: SEQ ID NO 42355
: LENGTH: 425
: TYPE: DNA
```


DB 798372 CCTATTTCACCAAAATATTCCTGCGCATGTTAAATTAAGAACTAGCATGAT 798313
QY 162 TCGTGTCCCTGACCCAA 180
DB 798312 TTCTTACTGGTGACCAA 798294

RESULT 11
US-09-634-306B-167810/c
; Sequence 167810, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 167810
; LENGTH: 824
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-167810

Query Match
Best Local Similarity 59.6%; Score 33.2; DB 27; Length 824;
Matches 56; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 76 AATGATGTAAGAAACCTTTATTAACCGGGTTTCGACAAACATCGCTAGATCAT 135
DB 384 ATATTAATGAGAAACCAAAAGAGTAACCAATATTTAAAGAAAGCTGAACATGATCTA 325

QY 136 TGATGACAACATGAGCTAAGCAAAAGTGTGTC 169
DB 324 TGATGACAACATGAGCTAAGCAAGGCTGTATATC 291

RESULT 12
US-10-027-632-167810/c
; Sequence 167810, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23

;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 167810
;; LENGTH: 824
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-167810

Query Match
Best Local Similarity 59.6%; Score 33.2; DB 44; Length 824;
Matches 56; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 76 AATGATGTAAGAAACCTTTATTAACCGGGTTTCGACAAACATCGCTAGATCAT 135
DB 384 ATATTAATGAGAAACCAAAAGAGTAACCAATATTTAAAGAAAGCTGAACATGATCTA 325

QY 136 TGATGACAACATGAGCTAAGCAAAAGTGTGTC 169
DB 324 TGATGACAACATGAGCTAAGCAAGGCTGTATATC 291

RESULT 13
US-60-207-422-55
; Sequence 55, Application US/60207422
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; FILE REFERENCE: C1000610
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 32768
; TYPE: DNA
; ORGANISM: HUMAN
; NAME/KEY: misc.feature
; LOCATION: (1)...(32768)
; OTHER INFORMATION: n - A,T,C or G
US-60-207-422-55

Query Match
Best Local Similarity 54.0%; Score 33.2; DB 74; Length 32768;
Matches 68; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 33 AGCATTAATCTGTGCTGATTCGCTATTTTCAATACCTTCGGGAAATGATGAAACC 92
DB 29509 AGCTAAATACGACCTTTTCATTTAAATAAGAAAGGAAATAAGAAAGAG 29568

QY 93 CTTATTAACCGGGTTTCGACAAACATCGCTAGTATCATTTGATGACCAATGAGACT 152
DB 29569 CCTGTAATCCAGAGCTTTGGGAGACTTAGCCAGAGAGATCATTTGAGATGCTTGAAGCT 29628

QY 153 AAGCAA 158
DB 29629 CAGGAA 29634

RESULT 14
US-09-528-237A-20/c
; Sequence 20, Application US/09528237A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
; TITLE OF INVENTION: Sequences and Uses Thereof


```
FILE REFERENCE: CL000284
CURRENT APPLICATION NUMBER: US/09/528.237A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 2926
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 133318
TYPE: DNA
ORGANISM: Drosophila
US-09-528-237A-20

Query Match
Best Local Similarity 17.3%; Score 33.2; DB 22; Length 133318;
Matches 53; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

26 CTGACAGCATATCTGTCTGATTCGCTATTTTCATATCCTTCGCGGGAATAGATGT 85
48226 CTCGACACGCAATATATTTCCGATTCGTTATTCGTAGACTTGGCTAAATGCTCA 48167
QY 86 GAAACCCCTATATAACGCGGCTTT 111
DB 48166 GAAAGCTCATAGATATATCGTTT 48141

RESULT 15
US-09-948-128-318/C
Sequence 318, Application US/09948128
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON CH
TITLE OF INVENTION: 17, METHODS OF DETECTION, AND USES THEREOF
FILE REFERENCE: CL001294
CURRENT APPLICATION NUMBER: US/09/948.128
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 465
SEQ ID NO 318
LENGTH: 12360069
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(12360069)
OTHER INFORMATION: n - A,T,C or G
US-09-948-128-318

Query Match
Best Local Similarity 17.1%; Score 32.8; DB 40; Length 12360069;
Matches 52; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

36 ATATCTTGTCGATTCGCTATTTTCATATCCTTCGCGGGAATAGATGTGAACCCCT 95
DB 7643639 AGATATTTCTTTTCACACCTACTGTATACCTCCGCGTAATAGCATGACATATA 7643580
QY 96 ATAAACGCGGCTTTTCGAGAAA 119
DB 7643579 ATGAATATCTTTTCTGAGAAA 7643556

Search completed: August 25, 2003, 21:54:32
Job time : 1571.9 secs
```

Gencore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 18:46:38 ; Search time 30.8534 Seconds
(without alignments)
2746.715 Million cell updates/sec

Title: US-09-816-391A-1_COPY_1_192
Perfect score: 192
Sequence: 1 gcctggcgccggcgccatga.....tgaccacaagaagatgcttt 192

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCUTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	29.8	15.5	10303	4 US-09-634-238-410	Sequence 410, App
C 2	29.2	15.2	3092	1 US-08-426-627-3	Sequence 3, Appl1
C 3	29.2	15.2	3126	2 US-08-477-396A-3	Sequence 3, Appl1
C 4	29.2	15.2	3253	1 US-08-426-627-5	Sequence 5, Appl1
C 5	29	15.1	1830121	4 US-09-557-884-1	Sequence 1, Appl1
C 6	29	15.1	1830121	4 US-09-643-990A-1	Sequence 1, Appl1
C 7	27.8	14.5	730	3 US-08-943-731-128	Sequence 128, App
C 8	27.8	14.5	1257	1 US-08-330-154-1	Sequence 1, Appl1
C 9	27.8	14.5	1269	4 US-09-134-001C-2393	Sequence 2393, Ap
C 10	27.8	14.5	24183	3 US-08-943-731-3	Sequence 3, Appl1
C 11	27.4	14.4	336	4 US-09-328-352-692	Sequence 692, App
C 12	27.4	14.3	7650	4 US-09-221-017B-911	Sequence 911, App
C 13	27.4	14.3	202001	4 US-09-734-674-3	Sequence 3, Appl1
C 14	27.4	14.3	580073	4 US-08-545-528D-1	Sequence 3017, Ap
C 15	27.2	14.2	318	4 US-09-107-532A-3017	Sequence 2248, Ap
C 16	27.2	14.2	615	4 US-09-107-532A-2248	Sequence 1, Appl1
C 17	27.2	14.2	168575	4 US-09-426-290-1	Sequence 1, Appl1
C 18	27	14.1	1009	6 5223394-8	Sequence 1, Appl1
C 19	27	14.1	1244	2 US-08-204-288-3	Sequence 12, Appl1
C 20	27	14.1	3182	1 US-08-188-582-12	Sequence 12, Appl1
C 21	27	14.1	3182	1 US-08-646-715-12	Sequence 12, Appl1
C 22	27	14.1	3852	1 US-08-306-546C-1	Sequence 1, Appl1
C 23	27	14.1	3852	2 US-08-530-524A-1	Sequence 1, Appl1
C 24	27	14.1	4321	4 US-09-773-426A-4	Sequence 4, Appl1
C 25	27	14.1	13993	4 US-09-220-132-20	Sequence 20, Appl1
C 26	27	14.1	14070	4 US-09-108-006C-2	Sequence 2, Appl1
C 27	26.8	14.0	875	4 US-09-221-017B-671	Sequence 671, App

C 28	26.8	14.0	1710	4 US-08-630-915A-189	Sequence 189, App
C 29	26.8	14.0	42571	4 US-09-810-347-3	Sequence 3, Appl1
C 30	26.6	13.9	3484	4 US-09-308-090-1	Sequence 1, Appl1
C 31	26.6	13.9	3484	4 US-09-380-090A-1	Sequence 1, Appl1
C 32	26.6	13.9	129908	4 US-09-585-858-1	Sequence 1, Appl1
C 33	26.4	13.7	927	4 US-09-328-352-2966	Sequence 2966, Ap
C 34	26.4	13.7	1230025	4 US-09-198-452A-1	Sequence 1, Appl1
C 35	26.2	13.6	924	4 US-09-107-532A-620	Sequence 620, App
C 36	26.2	13.6	1610	4 US-09-347-803-19	Sequence 19, Appl
C 37	26.2	13.6	2005	4 US-08-936-165A-102	Sequence 102, App
C 38	26.2	13.6	2559	4 US-09-071-035-325	Sequence 325, App
C 39	26.2	13.6	2559	4 US-09-071-035-329	Sequence 329, App
C 40	26.2	13.6	2559	4 US-09-071-035-333	Sequence 333, App
C 41	26.2	13.6	2801	3 US-08-747-221B-30	Sequence 30, Appl
C 42	26.2	13.6	2801	3 US-08-747-221B-32	Sequence 32, Appl
C 43	26.2	13.6	2801	3 US-09-005-051-30	Sequence 30, Appl
C 44	26.2	13.6	2801	3 US-09-005-051-32	Sequence 32, Appl
C 45	26.2	13.6	2836	3 US-08-747-221B-24	Sequence 24, Appl

ALIGNMENTS

```

RESULT 1
US-09-634-238-410/c
; Sequence 410, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christenson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.104301
; CURRENT APPLICATION NUMBER: US/09/634,238
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 410
; LENGTH: 10303
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-410

Query Match      15.5%; Score 29.8; DB 4; Length 10303;
Best Local Similarity 60.5%; Pred. No. 2;
Matches 49; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY      112 CGCGAAGACATGCGCTTGATGATGACACATGACCAAAAGTCTTGCC 171
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      8088 CGAAGAAAGCGAAGACATGTTGAAGATGATGACGAGCAAAAGATTGCGC 8029
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      172 CTGACCAAGAAAGATGCTTT 192
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      8028 CGGCTCGAAAGATGCGGCTTT 8008
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 2
US-08-426-627-3
; Sequence 3, Application US/08426627
; Patent No. 5756664
; GENERAL INFORMATION:
; APPLICANT: Amann, Egon
; APPLICANT: Atawara-Hanamoto, Yoko
; APPLICANT: Kikuno, Reiko
; APPLICANT: Takeshita, Sunao

```



```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,627
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/036,841
FILING DATE: 25-MAR-1993
APPLICATION NUMBER: JP 4-71501
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hammond, Alan W.
REGISTRATION NUMBER: 35,178
REFERENCE/DOCKET NUMBER: 02481-1285-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3253 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: osteosarcoma
FEATURE:
NAME/KEY: CDS
LOCATION: join(32..3540)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: join(97..2540)
US-08-426-627-5

Query Match      15.2%  Score 29.2; DB 1; Length 3253;
Best Local Similarity 59.8%; Pred. No. 2.1;
Matches 49; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY 89 AACCTATATAAACGGGGTTTGGCAGAAACATGCGCTATATCATGTGATGACAACTG 148
DB 620 AACCTATATCTTAATGGGGTTCATGCTTAATGCTGCAATCATCATGAGAACAC 679
OY 149 GACTAACCAAAAGTCTGTCC 170
DB 680 ATTGCACAACAATGCTGTGCC 701

RESULT 5
US-09-557-884-1/c
Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fieischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
```

```

CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
```

```

Query Match      15.1%  Score 29; DB 4; Length 1830121;
Best Local Similarity 53.0%; Pred. No. 28;
Matches 62; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

OY 31 CAACATATATCTTGTGCTATTCGCTATTTTCAATACCTTGGGGAATAGATGAAAA 90
DB 1014886 CACCAATATTAATTTGGATGCTTTATTTGAATTAATTTGATGAAAAATTTCTTGC 1014827
OY 91 CCCTATATAAACGGGGTTTTCGAGAAACATGCGCTAGTATCATGTGATGACAACT 147
DB 1014826 GCCATATACACGATGTGTTTTCATGAGCGTGTGATTAAGATTGATCTCCAAACT 1014770

RESULT 6
US-09-643-990A-1/c
Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: Robert D. Fieischmann
Mark D. Adams
Owen White
Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
```

FILED DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1
Query Match 15.1%; Score 29; DB 4; Length 1830121;
Best Local Similarity 53.0%; Pred. No. 28;
Matches 62; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 31 CAAGCATATCTGTCTGATTCGTATTTCAATACCTTCGGGAAATGATGTGAAA 90
DB 1014886 CACCCAAATTAATTTGGATGGTTTATTTGATTAATATGATGAAATTAATCTTGC 1014827
QY 91 CCCTTATTAACCGCGGCTTTCGACAGAAACGCGCATGATCATGATGACAAAT 147
DB 1014826 GCCATATACAGATGTTTTCATGAGCGTGAATTAATCTGATCTCCAAAT 1014770
RESULT 7
US-09-943-731-128/C
Sequence 128, Application US/08943731
Patent No. 6265157
GENERAL INFORMATION:
APPLICANT: PROCKOP, DARWIN J.
APPLICANT: SPOTILA, LORETTA D.
APPLICANT: DELTAS, CONSTANTINOS D.
APPLICANT: SEREDA, LARISA
APPLICANT: LARSON, ANDREA W.
APPLICANT: PACK, MICHAEL
APPLICANT: COLIGE, ALAIN
APPLICANT: EARLY, JAMES
APPLICANT: KORRKO, JARMO
APPLICANT: ALA-KORRKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
NUMBER OF SEQUENCES: 666
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADDEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: FLR.
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322

FILED DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9598-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 730 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-943-731-128
Query Match 14.5%; Score 27.8; DB 3; Length 730;
Best Local Similarity 65.1%; Pred. No. 3.5;
Matches 41; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 130 TATCATGATGACATGACTGACCTTACCAAGTCTTCCCTGACCAAGAGATGC 189
DB 374 TTTCAGAGTACGACCTTGACCAAGCTGCTATCCCTGCTGAAAGCTGC 315
QY 190 TTT 192
DB 314 TCT 312
RESULT 8
US-08-330-154-1
Sequence 1, Application US/08330154
Patent No. 5587307
GENERAL INFORMATION:
APPLICANT: Alborn Jr., William E
APPLICANT: Hoskins, Joann L
APPLICANT: Skatrud, Paul L
APPLICANT: Unal, Serhat
TITLE OF INVENTION: FEM A GENE OF STAPHYLOCOCCUS EPIDERMIDIS,
TITLE OF INVENTION: THE FEM A GENE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Division/AEH
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,154
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/208,925
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US/08/057,163
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hamilton, Amy E
REGISTRATION NUMBER: 33,894
REFERENCE/DOCKET NUMBER: X-8894
TELECOMMUNICATION INFORMATION:

TELEPHONE: 317-276-3169
TELEFAX: 317-276-1294
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1257
US-08-330-154-1

Query Match 14.5%; Score 27.8; DB 1; Length 1257;
Best Local Similarity 62.0%; Pred. No. 4.4;

Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 89 AACCCCTATTAAGCGGTTTCGAGAAACATGCGCTATATCATGATGACACATG 148
DB 694 AAACATTAATAAGACCGGTGTTTAGTACCACTAGCCTATATTACTTGTGATGATATA 753
QY 149 GACTAAGCAA 159
DB 754 GAGGAACATAA 764

RESULT 9

US-09-134-001C-2393
Sequence 2393, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stramm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

PRIOR FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 2393

LENGTH: 1269

TYPE: DNA

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-2393

Query Match 14.5%; Score 27.8; DB 4; Length 1269;
Best Local Similarity 62.0%; Pred. No. 4.4;

Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 89 AACCCCTATTAAGCGGTTTCGAGAAACATGCGCTATATCATGATGACACATG 148
DB 703 AAACATTAATAAGACCGGTGTTTAGTACCACTAGCCTATATTACTTGTGATGATATA 762
QY 149 GACTAAGCAA 159
DB 763 GAGGAACATAA 773

RESULT 10

US-08-943-731-3/c
Sequence 3, Application US/08943731
Patent No. 6265157

GENERAL INFORMATION:

APPLICANT: PROCKOP, DARWIN J.

APPLICANT: SPOTILA, LORETTA D.

APPLICANT: DETTAS, CONSTANTINOS D.

APPLICANT: SEREDA, LARISSA

APPLICANT: LARSON, ANDREA W.

APPLICANT: PACK, MICHAEL

APPLICANT: COLIGE, ALAIN
APPLICANT: EARLY, JAMES
APPLICANT: KORKKO, JARMO
APPLICANT: ALA-KORKKO, LEENA, et al
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
NUMBER OF SEQUENCES: 666
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & MANDEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: FLR
CITY: PHILADELPHIA
STATE: PA

COUNTRY: USA
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322

FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628

FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN

REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9598-27

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991

TELEX: 831-494
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 24183 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-943-731-3

Query Match 14.5%; Score 27.8; DB 3; Length 24183;
Best Local Similarity 65.1%; Pred. No. 14;

Matches 41; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 130 TATCATTTGATGACACATGAGTAAAGTGTTCCTCCCTACCCAGAACAGATGC 189
DB 10606 TTTCGAAGTGCACACCTTGACCAAGCTAGCTAGCTATCCCTCGAAGGCTGC 10547
QY 190 TTT 192
DB 10546 TCT 10544

RESULT 11

US-09-328-352-692/c
Sequence 692, Application US/09328352
Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 692

Job time : 38.8534 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 18:46:38 ; Search time 96.4169 Seconds
(without alignments)
2746.715 Million cell updates/sec

Title: US-09-816-391A-1

Perfect score: 600

Sequence: 1 gctggcgcgcgcgcatga.....tattcgactagtcgacg 600

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/prodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCUS.COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67.2	11.2	363	US-09-252-991A-7263	Sequence 7263, Ap
2	65.6	10.9	426	US-09-252-991A-13810	Sequence 13810, A
3	64.2	10.7	312	US-09-252-991A-13634	Sequence 13634, A
4	63.4	10.6	312	US-09-252-991A-13917	Sequence 13917, A
5	46.8	7.8	477	US-09-252-991A-3732	Sequence 3732, Ap
6	46.8	7.8	567	US-09-252-991A-3828	Sequence 3828, Ap
7	43.6	7.3	16075	US-09-096-942-1	Sequence 1, Appl1
8	43.6	7.3	16075	US-09-096-867-1	Sequence 1, Appl1
9	42	7.0	306	US-09-252-991A-14703	Sequence 14703, A
10	42	7.0	498	US-09-252-991A-15197	Sequence 15197, A
11	40.6	6.8	732	US-09-252-991A-8860	Sequence 8860, Ap
12	40.6	6.8	1047	US-09-252-991A-9034	Sequence 9034, Ap
13	40.6	6.8	1464	US-09-252-991A-8971	Sequence 8971, Ap
14	40.6	6.8	1494	US-09-252-991A-9117	Sequence 9117, Ap
15	39.6	6.6	2178	US-09-252-991A-7630	Sequence 7630, Ap
16	39.6	6.6	3030	US-09-252-991A-7921	Sequence 7921, Ap
17	39.6	6.6	4403765	US-09-103-840A-2	Sequence 2, Appl1
18	39.6	6.6	4411529	US-09-103-840A-1	Sequence 1, Appl1
19	38.4	6.4	765	US-09-252-991A-4768	Sequence 4768, Ap
20	38.4	6.4	1047	US-09-252-991A-4739	Sequence 4739, Ap
21	37.8	6.3	309	US-09-252-991A-12150	Sequence 12150, A
22	37.6	6.3	858	US-09-095-855-200	Sequence 200, App
23	37.6	6.3	858	US-09-205-426-200	Sequence 200, App
24	37.4	6.2	555	US-09-252-991A-11170	Sequence 11170, A
25	37.4	6.2	969	US-09-199-637A-48	Sequence 48, Appl
26	37.4	6.2	1017	US-09-199-637A-46	Sequence 46, Appl
27	37.4	6.2	1083	US-09-252-991A-11841	Sequence 11841, A

28	37.4	6.2	1407	US-09-252-991A-11543	Sequence 11543, A
29	37.4	6.2	1608	US-09-252-991A-11665	Sequence 11665, A
30	37.4	6.2	2025	US-09-199-637A-50	Sequence 50, Appl
31	37.4	6.2	2304	US-09-252-991A-11691	Sequence 11691, A
32	37.4	6.2	42235	US-09-199-637A-1	Sequence 1, Appl1
33	37.2	6.2	1428	US-09-252-991A-2357	Sequence 2357, Ap
34	37.2	6.2	1449	US-09-252-991A-2559	Sequence 2559, Ap
35	37.2	6.2	2343	US-09-252-991A-2275	Sequence 2275, Ap
36	37	6.2	2943	US-08-042-747A-7	Sequence 7, Appl1
37	36.6	6.1	77536	US-09-410-551B-1	Sequence 1, Appl1
38	36.6	6.1	4403765	US-09-103-840A-2	Sequence 2, Appl1
39	36.6	6.1	4411529	US-09-103-840A-1	Sequence 1, Appl1
40	36.2	6.0	375	US-09-199-637A-52	Sequence 52, Appl
41	35.4	5.9	666	US-09-252-991A-10065	Sequence 10065, A
42	35.4	5.9	711	US-09-252-991A-12233	Sequence 12233, A
43	35.4	5.9	876	US-09-252-991A-9769	Sequence 9769, Ap
44	35.4	5.9	1095	US-09-252-991A-12376	Sequence 12376, Ap
45	35.4	5.9	1188	US-09-252-991A-12167	Sequence 12167, A

ALIGNMENTS

```

RESULT 1
US-09-252-991A-7263
; Sequence 7263, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7263
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7263

Query Match
Best Local Similarity 53.4%; Score 67.2; DB 4; Length 363;
Matches 141; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

205 AAGTCTGACCTGTTTCGAAGATGCGCCGAGAGTCAACCTGACCAAGCTCAGCGGAG
97 AAACGAGAACTAAGCCGCGCTATGCGGAAAGCGGATCTCACCAGAAACAGCCGCAAT
265 GCTGCTGTTAAGCCCTTCAGAGATGTTCTCGAGGCTAGTGAAGTCCGGGAGGCTG
157 CGCTTCACACGCGCCGCTGATGATGAATACCGCGCGCTGAAACCGAAGAGAGCTG
325 AAGTCACCGGCGCTGTTCTCGCTGAGCGGCTCAAGCGCGGCTGACCGCGGCAAC
217 ACCCTGCTGCTTTCGCGACCTTCCTGCAACGCCATCGCGGAGCCGACAGAGAAAG
385 CCGGCACTGGCGAGCATTTGACATTCGCGCTTCACGCGCTTCATCTCCGCTGCG
277 CCGGAGACCGGCGCGCGGTGATGAATTAAGCCAGCAACCGTCCGCTTCAAGCCGCGG
445 TCCCTGCTGAAGAGCGCGTCAAC 468
337 AAGCCCTCGCGCGCGCGGTCAAC 360

RESULT 2
US-09-252-991A-13810/c
; Sequence 13810, Application US/09252991A

```

```

: Patent No. 6551795
: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OR INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OR INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 1071966.136
: CURRENT APPLICATION NUMBER: US/09/252,991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 3142
: SEQ ID NO 13810
: LENGTH: 426
: TYPE: DNA
: ORGANISM: Pseudomonas aeruginosa
: US-09-252-991A-13810

```

[illegible]

```

RESULT 3
US-09-252-991A-13634
; Sequence 13634, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13634
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13634

```

	Query Match	Similarity	Score	DB	Length
DB	Best Local	Similarity	52.4%	Pred No. 4,5e-10	
	Matches	141;	Conservative	0;	Mismatches 128; Indels 0; Gaps 0;
07	202	AACAAGTGTACCTCGTTTCCGAAGATGCGCCAGAAATCCACCTGACCAAGGCTCAAGGC	261		
DB	43	AACAAGTGTGGAACATATGATGCAATTTGCCGCGATCGCTGCAATATCCCGAAATCGTTGGC	102		

[illegible]

RESULT 4
 US-09-252-991A-13917/c
 : Sequence 13917, Application US/09252991A
 : Patent No. 6551795
 : GENERAL INFORMATION:
 : APPLICANT: Marc J. Rubenfield et al.
 : TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
 : FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 : FILE REFERENCE: 107196.136
 : CURRENT APPLICATION NUMBER: US/09/252,991A
 : CURRENT FILING DATE: 1999-02-18
 : PRIOR APPLICATION NUMBER: US 60/074,788
 : PRIOR FILING DATE: 1998-02-18
 : PRIOR APPLICATION NUMBER: US 60/094,190
 : PRIOR FILING DATE: 1998-07-27
 : NUMBER OF SEQ ID NOS: 33142
 : SEQ ID NO 13917
 : LENGTH: 312
 : TYPE: DNA
 : ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-991A-13917

Query Match	10.6%	Score 63.4	DB 4	Length 312
Best Local Similarity	52.5%	Pred. No. 7.9-10		
Matches 139	Conservative 0	Mismatches 126	Indels 0	Gaps 0
QY	202	AACAAGTGCACCTCGTTTCGAAAGTCCCGCCAGAAATGCCAAGATCCAGACCTGACCAAGCTCAGGCC	261	
Db	266	AACAATCCGGAAGCTGATGCATGCAATTCGCCCAATTCGTGTATATCCGAAGATGTTGCC	207	
QY	262	GAGCGTGTGTTAAGCGCTTCCTCCAGATGTGTGTCTGCAGGTATGAAGTCCGGCGGAAGC	321	
Db	206	GTTCGGGCACTGGAGCGCAATGATTCGAATGCCATCGGCGCCCTGAAGGCTGGTGACTCC	147	
QY	322	CTGAAGCTCAACGGGCTGTCTTCCGCTTAAGCGGTCAAGCGCCCGGTGCACACGGGCGC	381	
Db	146	GTGTCTGTGGTGTGTTTGGCACCTTCCTCTGCATTAAGAGCGCGGTGTCTGCACCGGTGC	87	
QY	382	AACCCGCGGACTGCGGAGCAGATGATTCACATTCGCGTTCCTAACGGCGTTCTATCTCCGCT	441	
Db	86	AACCCGGAAGCTGCACAGCCGATCAAGATTCGCGGTCCGCTCAAGATCCGGGCTTCAAGCC	27	
QY	442	GGCTCCCTGCTGAAGAAGGCCCTCA	466	
Db	26	GGTAAAGCCCTGAAGGATGCTGTCA	2	

RESULT 5
 US-09-252-991A-3732
 ; Sequence 3732, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

```

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3732
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3732

```

Query Match 7.8%; Score 46.8; DB 4; Length 477;
Best Local Similarity 47.9%; Pred. No. 0.00011;

Matches 135; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

```

QY 193 ATGGCAATACAAAGTCTGACCTGTTTGAAGATCGCCCAAGAGTCCAGTCCAGCAG 252
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 196 ATGGCACTGACCAAGAACCAAGTATCCAGAGATGCGCCAGAACCTCGACGCGCAGAG 255
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 253 GCTCAGCGCGAGGCTCTGTAAAGCCTTCAGAGATGTGTTGTCGAGGCTATGAATCC 312
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 256 ACCACCGTTCGACGCGCTCGACAGCTCGCCGAGATGTCAGAGACGCCCTGAGAGAC 315
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 313 GCGCAAGGCTGAGAGTCAACGCGGCTGTCTCCGTCGAGCGGCTCAAGCGCGGCTCG 372
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 316 GATGGCGAATACACCTGCGCGGATGCGCAAGCTGAAGTCTCCGAGGTCGCCGCGC 375
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 373 ACCGCGCGCAACCCGCGGACTGCGGAGCAGATTGACATTCGCGCTCTACGCGCTCG 432
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 376 ACCGCGCGCAACCCGCGGAGCAGAGCGCAAGGATGAGATGCTGCCAAGGCTGAGCCAG 435
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 433 ATCTCGCTGGCTCCTCTGTGAAGAGCGGCTCACCGAGTGA 474
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 436 TTCGTTCCGCGCAAGGCACTGACCGAGCATCAACGCGCTGA 477
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

RESULT 6

```

US-09-252-991A-3828/c
; Sequence 3828, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3828
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3828

```

Query Match 7.8%; Score 46.8; DB 4; Length 567;
Best Local Similarity 47.9%; Pred. No. 0.00011;

Matches 135; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

```

QY 193 ATGGCAATACAAAGTCTGACCTGTTTGAAGATCGCCCAAGAGTCCAGTCCAGCAG 252
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 557 ATGGCACTGACCAAGAACCAAGTATCCAGAGATGCGCCAGAACCTCGACGCGCAGAG 498
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 253 GCTCAGCGCGAGGCTCTGTAAAGCCTTCAGAGATGTGTTGTCGAGGCTATGAATCC 312
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 497 ACCACCGTTCGACGCGCTCGACAGCTCGCCGAGATGTCAGAGACGCCCTGAGAGAC 438
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

```

QY 313 GCGCAAGGCTGAGAGTCAACGCGGCTGTCTCCGTCGAGCGGCTCAAGCGCGGCTCG 372
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 437 GATGGCGAATACACCTGCGCGGATGCGCAAGTCTCCGAGAGTCTCCGCGCGC 378
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 373 ACCGCGCGCAACCCGCGGACTGCGGAGCAGATTGACATTCGCGCTTCTCAAGCGGTTCT 432
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 377 ACCGCGCGCAACCCGCGGAGCAGAGCGCAAGGCGATGAGATCTCTCCCAAGCGTGAAGCAG 318
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 433 ATCTCGCTGGCTCCTCTGTGAAGAGCGGCTCACCGAGTGA 474
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 317 TTCGTTCCGCGCAAGGCACTGACCGAGCATCAACGCGCTGA 276
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

RESULT 7

```

US-09-096-942-1
; Sequence 1, Application US/09096942
; Patent No. 6027925
; GENERAL INFORMATION:
; APPLICANT: Pollock, Thomas J
; APPLICANT: Mikolajczak, Marcia
; APPLICANT: Yamazaki, Motohide
; APPLICANT: Armentrout, Richard W
; TITLE OF INVENTION: Production of Xanthan Gum by Sphingomonas Bacteria
; FILE REFERENCE: seq list for appl filed from pro. appl
; CURRENT APPLICATION NUMBER: US/09/096,942
; PRIOR FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 60/049,428
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 16075
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
; PUBLICATION INFORMATION:
US-09-096-942-1

```

Query Match 7.3%; Score 43.6; DB 3; Length 16075;
Best Local Similarity 47.7%; Pred. No. 0.0047;

Matches 127; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

```

QY 193 ATGGCAATACAAAGTCTGACCTGTTTGAAGATCGCCCAAGAGTCCAGTCCAGCAG 252
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 33 ATGGATGAGAGAAAGCGAGATGCGGAGCGTCTGTGACGAGATGCGGCTGAAACAG 92
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 253 GCTCAGCGCGAGGCTCTGTAAAGCCTTCAGAGATGTGTTGTCGAGGCTATGAATCC 312
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 93 CGTAGGCGGAGGAATTCGTGACGCGGTTTTCGATGTGCTGCGGAGTGCACCTGAGACAG 152
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 313 GCGCAAGGCTGAGAGTCAACGCGGCTGTCTCCGTCGAGCGGCTCAAGCGCGGCTCG 372
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 153 GCGCGTAGGTGAAGTGTGCGGCTTCGCGCAACTTCATCTGCGGCGCAAGAACCAAGCG 212
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 373 ACCGCGCGCAACCCGCGGACTGCGGAGCAGATTGACATTCGCGGCTTCTCAAGCGGTTCT 432
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 213 CCGGTCGCAATCCCAAGAGCGGAGGAAATTCGATCTGCGGAGAGAGCGGTGATACC 272
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 433 ATCTCGCTGGCTCCTCTGTGAAGAGCGGCTCACCGAGTGA 458
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 273 TTCGTTCCGCGCAAGGCACTGACCGAGCATCAACGCGCTGA 298
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

RESULT 8

```

US-09-096-867-1
; Sequence 1, Application US/09096867
; Patent No. 6030817
; GENERAL INFORMATION:
; APPLICANT: Pollock, Thomas J
; APPLICANT: Mikolajczak, Marcia
; APPLICANT: Yamazaki, Motohide
; APPLICANT: Thorne, Linda

```



```
FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252,991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 7630
: LENGTH: 2178
: TYPE: DNA
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7630

Query Match      6.68; Score 39.6; DB 4; Length 2178;
Best Local Similarity 60.08; Pred. No. 0.032;
Matches 66; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

OY 272 TTAACGCTTCAGAGATGTGTGCGAGGCTATGAGTCGCGGCAAGGCTGAAGCTCA 331
   ||||| ||||| || ||||| || ||||| ||||| ||||| ||||| |||||
Db 1880 TCAACGATTTACCAAGCCCTTGCAGCGCCCGCCCTGTACGACAGCAATGGGCTGATGCTGG 1821
   ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||

OY 332 CCGGCTGTCTCCGCTGAGCGCGCTCAAGCGCCCGGCTCGACCGGCGC 381
   ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db 1820 CCGACCTGCAACGCGGCGGACACCTCAAGCTGCCGCGCCGCTGACCGC 1771
   ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
```

Search completed: August 25, 2003, 19:52:13
Job time : 106.417 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 18:56:32 ; Search time 230.619 Seconds

(without alignments)
5849.036 Million cell updates/sec

Title: US-09-816-391A-1

Perfect score: 600
Sequence: 1 gctggcgccgagcgcacatga.....tattccgactagcttcacgcg 600

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PC7_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PC7US_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	600	100.0	600	9	US-09-816-391A-1
2	77.6	12.9	279	14	US-10-156-761-5111
3	77.6	12.9	90235608	14	US-10-156-761-1
4	68.8	11.5	273	14	US-10-127-032-71
5	64.2	10.7	273	9	US-09-815-242-7753
6	61.8	10.3	651	14	US-10-156-761-2671
7	61.8	10.3	9025608	14	US-10-156-761-1
8	48.2	8.0	273	9	US-09-815-242-9847
9	41.8	7.0	273	9	US-09-815-242-5974
10	39	6.5	1326	10	US-09-749-7288-12
11	39	6.5	3411	14	US-10-156-761-5111
12	38.4	6.4	696	9	US-09-815-242-9847
13	37.6	6.3	858	12	US-10-205-979-26
14	37.6	6.3	858	13	US-10-051-643-200
15	37.6	6.3	1089	14	US-10-156-761-6834
16	37.4	6.2	447	9	US-09-864-761-27737

17	37.4	6.2	969	11	US-09-975-719-48	Sequence 48, Appl
18	37.4	6.2	1017	11	US-09-975-719-46	Sequence 46, Appl
19	37.4	6.2	2025	11	US-09-975-719-50	Sequence 50, Appl
20	37.4	6.2	17290	11	US-09-999-121-7	Sequence 7, Appl1
21	37.4	6.2	25760	11	US-09-999-121-13	Sequence 13, Appl1
22	37.4	6.2	42235	11	US-09-975-719-1	Sequence 1, Appl1
23	37.2	6.2	1395	9	US-09-815-242-8008	Sequence 8008, Ap
24	37	6.2	1830	14	US-10-081-872-181	Sequence 181, Ap
25	37	6.2	2423	13	US-10-108-605-320	Sequence 320, Ap
26	36.8	6.1	657	9	US-09-815-242-3785	Sequence 3785, Ap
27	36.6	6.1	385	9	US-09-864-761-11106	Sequence 11106, A
28	36.6	6.1	1317	14	US-10-156-761-4093	Sequence 4093, Ap
29	36.6	6.1	1425	14	US-10-156-761-3327	Sequence 3327, Ap
30	36.6	6.1	1830	14	US-10-081-872-181	Sequence 181, Ap
31	36.2	6.0	276	9	US-09-815-242-9221	Sequence 9221, Ap
32	36.2	6.0	375	11	US-09-975-719-52	Sequence 52, Appl
33	36	6.0	1002	14	US-10-156-761-2166	Sequence 2166, Ap
34	36	6.0	1299	14	US-10-156-761-2376	Sequence 2376, Ap
35	35.6	5.9	765	14	US-10-156-761-7195	Sequence 7195, Ap
36	35.4	5.9	1491	14	US-10-156-761-1868	Sequence 1868, Ap
37	35.2	5.9	669	14	US-10-156-761-213	Sequence 213, Ap
38	35.2	5.9	996	9	US-09-815-242-7775	Sequence 7775, Ap
39	35.2	5.9	1020	14	US-10-156-761-3960	Sequence 3960, Ap
40	35.2	5.9	4512	14	US-10-156-761-2222	Sequence 2222, Ap
41	35	5.8	1428	14	US-10-156-761-3841	Sequence 3841, Ap
42	34.8	5.8	876	14	US-10-156-761-7128	Sequence 7128, Ap
43	34.8	5.8	1086	14	US-10-156-761-3194	Sequence 3194, Ap
44	34.8	5.8	1281	14	US-10-156-761-3352	Sequence 3352, Ap
45	34.6	5.8	396	14	US-10-156-761-2292	Sequence 2292, Ap

ALIGNMENTS

RESULT 1
US-09-816-391A-1
Sequence 1, Application US/09816391A
Patent No. US20020054865A1
GENERAL INFORMATION:
APPLICANT: FUJIMORI, Minoru
APPLICANT: TANIGUCHI, Shunichiro
APPLICANT: AMANO, Jun
APPLICANT: YAZAWA, Kazuyuki
APPLICANT: KANO, Yasunobu
APPLICANT: NAKAMURA, Toshiyuki
APPLICANT: SASAKI, Takayuki
TITLE OF INVENTION: Anaerobic bacterium as a drug for cancer gene therapy
FILE REFERENCE: 2001-WM/C/01736
CURRENT APPLICATION NUMBER: US/09/816,391A
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 00/287688
PRIOR FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 1
LENGTH: 600
TYPE: DNA
ORGANISM: Bifidobacterium longum
FEATURE:
NAME/KEY: CDS
LOCATION: (193)..(471)
US-09-816-391A-1

Query Match 100.0%; Score 600; DB 9; Length 600;
Best Local Similarity 100.0%; Pred. No. 76-194;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GCTGGCGCGCGCGCCATGAGTGGCTTGACAGCATATCTGTCGATCGCTATTT	60
DB	1	GCTGGCGCGCGCGCCATGAGTGGCTTGACAGCATATCTGTCGATCGCTATTT	60
QY	61	TCAATCCTTGGGGAATGATGTGAAAACCTTTTAAACCGGGGTTTGCAGCAAC	120
DB	61	TCAATCCTTGGGGAATGATGTGAAAACCTTTTAAACCGGGGTTTGCAGCAAC	120

OY	122	ATGCGGTATACATTGATGAGACAAATGAGCAAGCAAAATCGTTTCCCTCCATGCCAA	180
	121	ATGCGGTATACATTGATGAGCAAAATGAGCAAGCAAAATCGTTTCCCTCCATGCCAA	180
Db	181	GAAGATGCTTTATGCGATACAAACAAGTCGACCTCGTTTCGAAGATGCGCCAGAAATCC	240
OY	181	GAAGATGCTTTATGCGATACAAACAAGTCGACCTCGTTTCGAAGATGCGCCAGAAATCC	240
Db	181	GAAAGATGCTTTATGCGATACAAACAAGTCGACCTCGTTTCGAAGATGCGCCAGAAATCC	240
OY	241	AACCTGACCAAGGCTCAGGCGGAGGCTGCTGTAAAGCGCTTCGAGATGCTGTGAG	300
Db	241	AACCTGACCAAGGCTCAGGCGGAGGCTGCTGTAAAGCGCTTCGAGATGCTGTGAG	300
OY	301	GCTATGAATCGCGGAGGAGGCTGGAAGCTCAACGGGCTGTTCGCTCGCTGAGCGGCTCAG	360
Db	301	GCTATGAATCGCGGAGGAGGCTGGAAGCTCAACGGGCTGTTCGCTCGCTGAGCGGCTCAG	360
OY	361	CGCGCGGCTCGCAACGGGCGCAACCCGGGCACTGGCGGAGAGATTGACATTCCGGGCTTCC	420
Db	361	CGCGCGGCTCGCAACGGGCGCAACCCGGGCACTGGCGGAGAGATTGACATTCCGGGCTTCC	420
OY	421	TACGGGCTTCGATCTCGCTGGCTCCCTCGCTGGAAGAAGCGCTGACCGAGTACCTTCT	480
Db	421	TACGGGCTTCGATCTCGCTGGCTCCCTCGCTGGAAGAAGCGCTGACCGAGTACCTTCT	480
OY	481	GCTCGTAGCGATTACTTGACGACCTTACAGACAAAGACCCCGACCGAGATGGTCCGGG	540
Db	481	GCTCGTAGCGATTACTTGACGACCTTACAGACAAAGACCCCGACCGAGATGGTCCGGG	540
OY	541	TCTTTTGTGTTGGGCGCTGACGCGTTGTCCAAACGATTAATTCGCGAGTACGTTCAAGC	600
Db	541	TCTTTTGTGTTGGGCGCTGACGCGTTGTCCAAACGATTAATTCGCGAGTACGTTCAAGC	600

```

1      RESULT 2
2      US-10-156-761-5111
3      ; Sequence 5111, Application US/10156761
4      ; Publication No. US20030119018A1
5      ;
6      ; GENERAL INFORMATION:
7      ;
8      ; APPLICANT: OMURA, SATOSHI
9      ; APPLICANT: IKEDA, HARUO
10     ; APPLICANT: ISHIRAWA, JUN
11     ; APPLICANT: HORIKAWA, HIROSHI
12     ; APPLICANT: SHIBA, TADAYOSHI
13     ; APPLICANT: SAKAKI, YOSHIYUKI
14     ; APPLICANT: HATTORI, MASAHIRA
15     ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
16     ; FILE REFERENCE: 249-262
17     ;
18     ; CURRENT APPLICATION NUMBER: US/10/156,761
19     ; CURRENT FILING DATE: 2002-05-29
20     ; PRIOR APPLICATION NUMBER: JP 2001-204089
21     ; PRIOR FILING DATE: 2001-05-30
22     ; PRIOR APPLICATION NUMBER: JP 2001-272697
23     ; PRIOR FILING DATE: 2001-08-02
24     ; NUMBER OF SEQ ID NOS: 15109
25     ;
26     ; SEQ ID NO 5111
27     ;
28     ; LENGTH: 279
29     ;
30     ; TYPE: DNA
31     ;
32     ; ORGANISM: Streptomyces avermitilis
33     ;
34     ; FEATURE:
35     ;
36     ; NAME/KEY: CDS
37     ; LOCATION: (1)..(279)
38     ;
39     ; US-10-156-761-5111

```

	12.9%	Score 77.6	DB 14	Length 279
Query Match Similarity	58.8%	Pred. 10.6	2e-16	
Best Local Similarity	153	Conservative	0	Mismatches 104; Indels 3; Gaps 1
OY	210	TGACCTCGTTTCGAAATGCGCCGACGAAGTCAACTGACCCAAAGCTCAGCGCGGAGGTGC	265	
DB	12	TGAGCTGCTGAGCGCGCCCTGCGACCGCGCCGACGAGGTGACCGCCGACGAGCGCGCGCT	71	
OY	270	TGTTAAGCGCCCTTCACGAGATGCTGTCGACAG--GCTATGAGTGTCCGCGGAGGCTTGAA	328	

Accession	Sequence	Position
Db	72 TCTGGCCGCGCTTGGCCGAGACCGCGCGGAGATCGTTGCCAAGGGCCAGCAGAAAGTTCAC	131
OY	327 GCTACACCGGCGCTTCTCCGCTGAGCGCGTCAGACGCCCGCGCCACACC	386
Db	132 CATCCCGCGGCTTCTGACCTTCGAGCGCCACCAACCGCGCGCGCACCGCGCTAAC	191
OY	387 GCGCACTGGGAGAGATTGACATTCGCGGCTTCCTACGGGCTTCGTACTCCGCTGCTC	446
Db	192 GCAACACGGGAGACCGATCCAGATCCCGGGGCTACAGGCTCAAGTCTTCGCGGGCTC	251
OY	447 CCTGCTAGAGAGGCGCTCA	466
Db	252 GAAGCTCAAGAAAGCGCCA	271

```

RESULT 3
US-10-156-761-1
: Sequence 1, Application US/10156761
: Publication NO. US20030119018A1
: GENERAL INFORMATION:
: APPLICANT: OMURA, SATOSHI
: APPLICANT: IKEDA, HARUO
: APPLICANT: ISHIKAWA, JUN
: APPLICANT: HORIKAWA, HIROSHI
: APPLICANT: SHIBA, TADATOSHI
: APPLICANT: SAKAKI, YOSHIYUKI
: APPLICANT: HATTORI, MASAHIRA
: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
: FILE REFERENCE: 249-262
: CURRENT APPLICATION NUMBER: US/10/156,761
: CURRENT FILING DATE: 2002-05-29
: PRIOR APPLICATION NUMBER: JP 2001-204089
: PRIOR FILING DATE: 2001-05-30
: PRIOR APPLICATION NUMBER: JP 2001-272697
: PRIOR FILING DATE: 2001-08-02
: NUMBER OF SEQ ID NOS: 15109
: SEQ ID NO 1
: LENGTH: 9025608
: TYPE: DNA
: ORGANISM: Streptomyces avermitilis
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: (4187715)
: OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

```

	Query Match	Best Local Similarity	12.9%;	Score 77.6;	DB 14;	Length 9025608;	
	Matches	153;	Conservative	0;	Mismatches 104;	Indels 3;	Gaps 1;
OY	210	TGACCTCGTTTCGANGATCGGCCAGAAAGTCCACCTTGACCAAGCCTCAGGCCGAGGCTGC	269				
Db	6227520	TGACCTCGTTGGCCGCGCTGGCCGACCGCGCCGAGGTGACCCGCAAGGACGCGCGCGCT	6227579				
OY	270	TGTTAAGCGCCTTCAGGATGTGTCGTGAG---GCTATGAAGTCCGGCGAAGCGCTGAA	326				
Db	6227580	TCTGGCCGCGCTTCCGCGAGACCGTCCGGCAGATGTGTCCAAAGGCGAGAAAGGTATC	6227639				
OY	327	GCATCACCAGCCTGTTCTCCGCTAGCGCGCGTCAAGCCGCCCGCTGGCACCGGCCCAACC	386				
Db	6227640	CATCCCCGGGCTCTCTGACCTTCGAGCGCACCAACCGCTGCCCTGGACACCGCGCTAACCC	6227699				
OY	387	GCGCATGCGGAGAGATTTGACATTTCCGGCTTCCCTAGCGCTGTATCTCCGCTGAGCTC	446				
Db	6227700	GCAACCGGGGAGACCGATTCAGATCCCGGGGGGTATACAGCGTCAAGGTCTCCGGGGGCTC	6227755				
OY	447	CCTGCTGAAGAGGCGCTCA	466				
Db	6227760	GAAGCTCAAGGAAGCCGCCA	6227779				

RESULT 4

US-10-127-032-71
; Sequence 71, Application US/10127032
; Publication No. US20030113742A1
; GENERAL INFORMATION:
; APPLICANT: Whiteley, Marvin
; APPLICANT: Bangera, M. Gita
; APPLICANT: Lory, Stephen
; APPLICANT: Greenberg, Everett Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF
; FILE OF INVENTION: BIOFILM FORMATION
; FILE REFERENCE: 012-070CP
; CURRENT APPLICATION NUMBER: US/10/127,032
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/285,190
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/344,142
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-127-032-71

Query Match 11.5%; Score 68.8; DB 14; Length 273;
Best Local Similarity 53.8%; Pred. No. 6, 2e-13;
Matches 142; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

OY 205 AAGTGTGACCTGCTTTCGAAGATCGCCGAGAGTCCACCTGACCAAGGCTCAGGCGGAG 264
DB 7 AACACGACACTGACGCGCCGCTATCGCCGAGAAAGGCGGATCTACCAAGAACAGGCGCAT 66
OY 265 GCTGTGTAAACGCTTTCAGAGATGCTTCGTCGAGGCTATGATGATCGGCGAAGGCGCTG 324
DB 67 GCGGTTCACAGCGCCGCTGTTGATGAAACACCGGCGGCTGACCGCAAGGACAGCGTG 126
OY 325 AAGTACCGGCTGCTTCGCTGAGCGGCTGACAGCGGCGGCTGCGACGCGGCGGCGGCAAC 384
DB 127 ACCGTGCGGCTGTTGGGACACTTCCTGCAAGCCCATCGGCGGAGCCGCGGAGGAAGAAC 186
OY 385 CCGGCGACTGGGAGCAATGACATTCGCGCTTCTACGCGGCTTCTGATCTCCGCTGCG 444
DB 187 CCGGAGACCGGCGGACCGGTGAAATCAAGGCGGACCAACACCGTGGCTTCAAGCGGCG 246
OY 445 TCCGCTGAGAGAGGCGGCTGACC 468
DB 247 AAGCCCTGCGCGACGCGGTCAAC 270

RESULT 5

US-09-815-242-7753
; Sequence 7753, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELTRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7753
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(273)
US-09-815-242-7753

Query Match 10.7%; Score 64.2; DB 9; Length 273;
Best Local Similarity 52.4%; Pred. No. 2, 3e-11;
Matches 141; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

OY 202 AACAGTGTGACCTGCTTTCGAAGATCGCCGAGAGTCCACCTGACCAAGGCTCAGGCG 261
DB 4 AACAGTGTGACCTGCTTTCGAAGATCGCCGAGAGTCCACCTGACCAAGGCTCAGGCG 63
OY 262 GAGGCTGCTTTCGAAGATCGCTTTCGAAGATCGCTTTCGAAGATCGCTTTCGAAGATCG 321
DB 64 GCTGCGGCTGCTTTCGAAGATCGCTTTCGAAGATCGCTTTCGAAGATCGCTTTCGAAGATCG 123
OY 322 CTGAAGTACCGGCTGCTTTCGCTGAGCGGCTGACAGCGGCGGCTGCGACGCGGCGGCG 381
DB 124 GTCGTGCTGCTTTCGCTGAGCGGCTGACAGCGGCTGACAGCGGCGGCTGCGACGCGGCGG 183
OY 382 AACCGGCGGCTGCTTTCGCTGAGCGGCTGACAGCGGCTGACAGCGGCTGACAGCGGCGG 441
DB 184 AACCGGCGGCTGCTTTCGCTGAGCGGCTGACAGCGGCTGACAGCGGCTGACAGCGGCGG 243
OY 442 GGCCTGCTGCTTTCGCTGAGCGGCTGACAGCGGCTGACAGCGGCTGACAGCGGCGG 470
DB 244 GGTAAAGCCTGAGATGCTGTCACTA 272

RESULT 6

US-10-156-761-2671
; Sequence 2671, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIDA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2671
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)


```

: APPLICANT: Sakura, Satoshi
: APPLICANT: Okura, Kazuhiko
: APPLICANT: Gojo, Satoshi
: APPLICANT: Yamada, Toji
: TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIO
: FILE REFERENCE: 00766, 000043
: CURRENT APPLICATION NUMBER: US/09/749, 7288
: CURRENT FILING DATE: 2001-09-17
: PRIOR APPLICATION NUMBER: H11-372826
: PRIOR FILING DATE: 1999-12-28
: PRIOR APPLICATION NUMBER: PCT-JP00-01148
: PRIOR FILING DATE: 2000-02-28
: PRIOR APPLICATION NUMBER: PCT-JP00-07741
: PRIOR FILING DATE: 2000-11-02
: NUMBER OF SEQ ID NOS: 80
: SOFTWARE: PatentIn Ver.2.0
: SEQ ID NO 12
: LENGTH: 1326
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: OTHER INFORMATION: (1)..(1329)
US-09-749-7288-12

Query Match
Best Local Similarity 6.5%; Score 39; DB 10; Length 1326;
Matches 92; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

QY 235 AAGTCAACCTGACCAAGGCTCAGGCCGAGCGCTGCTTAAACGCTTCCAGATGTGTC 294
Db 566 AGGACCCGGCGCTGTCGAGAGGGCGCGCGAGGCGCGCGCGCTGCGGCGCCAGGAGCGGCGCC 507
QY 295 GTCGAGCTTATGAAGTCGCGCGGCGAAGGCTGAGCTAACCTACCGGCTGTCTCCGCTAGAGCC 354
Db 506 ACGTCGGCCATGTAAGCGCGGGGTAGGGGCTGTAG-TAGGAGCCCGCGGCGAAGCGCGCGCGCC 448
QY 355 GTCAAGCGCCCGGCGCTGCGACCGGCGCGCAACCCGCGACTGGCG 397
Db 447 GTACTGCTCGCGGCGCGCGCGAGCGCCGACCCGCGCGCTCCGCCG 405

RESULT 11
US-10-198-846-9872/c
: Sequence 9872, Application US/10198846
: Publication No. US2003009974A1
: GENERAL INFORMATION:
: APPLICANT: Lillie, James
: APPLICANT: Xu, Yongyao
: APPLICANT: Wang, Youzhen
: APPLICANT: Seilmann, Kathleen
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
: TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
: FILE REFERENCE: MRI-049
: CURRENT APPLICATION NUMBER: US/10/198, 846
: CURRENT FILING DATE: 2002-07-18
: PRIOR APPLICATION NUMBER: 60/306, 220
: PRIOR FILING DATE: 2001-07-18
: NUMBER OF SEQ ID NOS: 14084
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9872
: LENGTH: 3411
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1, 2, 3
: OTHER INFORMATION: n = A,T,C or G
US-10-198-846-9872

```



```

; SEQ ID NO 200
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
;
US-10-051-643-200

```

Query Match	6.38;	Score 37.6;	DB 13;	Length 858;
Best Local Similarity	46.38;	Pred. No. 0.051;		
Matches 124;	Conservative	0;	Mismatches 144;	Indels 0;
			Gaps	0;

[illegible]

RESULT 15
US-10-156-761-6834

```

? GENERAL INFORMATION:
? APPLICANT: OMODA, SATOSHI
? APPLICANT: IKEDA, HARUO
? APPLICANT: ISHIKAWA, JUN
? APPLICANT: HORIKAWA, HIROSHI
? APPLICANT: SHIBA, TADAYOSHI
? APPLICANT: SAKAKI, YOSHIYUKI
? APPLICANT: HATTORI, MASAHIRA
? TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
? FILE REFERENCE: 249-262
? CURRENT APPLICATION NUMBER: US/10/156,761
? CURRENT FILING DATE: 2002-05-29
? PRIOR APPLICATION NUMBER: JP 2001-204089
? PRIOR FILING DATE: 2001-05-30
? PRIOR APPLICATION NUMBER: JP 2001-272697
? PRIOR FILING DATE: 2001-08-02
? NUMBER OF SEQ ID NOS: 15109
? SEQ ID NO 6834
? LENGTH: 1089
? TYPE: DNA
? ORGANISM: Streptomyces avermitilis
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(1089)
? OS-10-156-761-6834

```

Query Match	6.3%	Score 37.6;	DB 14;	Length 1089;
Best Local Similarity	48.2%;	Pred. No. 0.058		
Matches 106; Conservative	0;	Mismatches 114;	Indels 0;	Gaps 0

QY	DB	QY
252	GGCTAGAGCGCGAGGCTGCTGTTAAAGCCTTCAGAGATGTTCTGTGAGGCTATGAAGTC	31.1
516	GGCGGTGACTGGCTGCGCGGTCAAGATTAAGTCTCCGGGCTCGCCGAGATCAATCAAGGC	31.1
312	CGGCGAAGGCGCTGAAGCTACCGGCGTCTTCTCCGCTAGCGCGCTCAAGCGCCCGGCTCG	37.1
576	CGGGCTTCATGCGCGAGCCGAGGCAATCTGGAAGCTATGAGAGGCGCAACCGCAAGGGGGCCG	63.5

[illegible]

```
Search completed: August 25, 2003, 22:04:19
Job time : 254.619 secs
```